

CC IsoId=Q9NQW8-2; Sequence=VSP_009742;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Expressed specifically in the retina.
 CC -!- DISASE: Defects in CNGB3 are a cause of achromatopsia 3 (ACHM3)
 CC [MIM:242300]; also known as Pingelapese blindness. ACHM3 is a
 CC congenital complete achromatopsia and is distinct from total
 CC colorblindness mainly because of the consistent concurrence of
 CC severe myopia.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 CC (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; AF272900; AAF86274.1; -; mRNA.
 CC EMBL; AF228520; AAF80179.1; ALT INIT; mRNA.
 CC Ensembl; ENSG00000170289; Homo sapiens.
 CC HGNC; HGNC:2153; CNGB3.
 CC MIM; 605080; -;
 CC MIM; 262300; -;
 CC GO; GO:0007165; P:signal transduction; NAS.
 CC GO; GO:0006810; P:transport; NAS.
 CC GO; GO:0007601; P:visual perception; TAS.
 CC InterPro; IPR000595; cNMP bd.
 CC InterPro; IPR005821; Ion Trans.
 CC InterPro; IPR001622; K+channel pore.
 CC Pfam; PF00027; cNMP binding; 1.
 CC Pfam; PF00520; Ion trans; 1.
 CC SMART; SM00100; cNMP; 1.
 CC PROSITE; PS00888; CNMP_BINDING_1; 1.
 CC PROSITE; PS00889; CNMP_BINDING_2; 1.
 CC PROSITE; PS00442; CNMP_BINDING_3; 1.
 CC Alternative splicing; cGMP; cGMP-binding; Disease mutation;
 CC Glycoprotein; Ion transport; Ionic channel; Multigene family;
 CC Nucleotide-binding; Polymorphism; Sensory transduction; Transmembrane;
 CC Transport; Vision.
 CC TOPO_DOM 1 216 Cytoplasmic (Potential).
 CC TRANSMEM 217 237 H1 (Potential).
 CC TOPO_DOM 238 250 Extracellular (Potential).
 CC TRANSMEM 251 271 H2 (Potential).
 CC TOPO_DOM 272 302 Cytoplasmic (Potential).
 CC TRANSMEM 303 323 H3 (Potential).
 CC TOPO_DOM 324 359 Extracellular (Potential).
 CC TRANSMEM 360 380 H4 (Potential).
 CC TOPO_DOM 381 417 Cytoplasmic (Potential).
 CC TRANSMEM 418 438 H5 (Potential).
 CC TOPO_DOM 439 504 Extracellular (Potential).
 CC TRANSMEM 505 525 H6 (Potential).
 CC TOPO_DOM 526 809 Cytoplasmic (Potential).
 CC NP_BIND 532 676 cGMP (By similarity).
 CC BINDING 592 592 cGMP (By similarity).
 CC BINDING 604 604 cGMP (By similarity).
 CC CARBOHYD 468 468 N-linked (GlcNAc...) (Potential).
 CC VARSPLIC 590 594 Missing (in isoform 2).
 CC FTID=VSP_009742.
 CC W -> C (in dbSNP:6471482).
 CC /FTID=VAR_018109.
 CC T -> P (in dbSNP:4961206).
 CC /FTID=VAR_018110.
 CC S -> F (in ACHM3).
 CC /FTID=VAR_018111.
 CC E -> G (in dbSNP:3735972).
 CC /FTID=VAR_018112.
 CC SEQUENCE 809 AA; 92250 MW; AC23B7072C1C7DB3 CRC64;
 CC
 CC Query Match 100.0%; Score 4234; DB 1; Length 809;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e-238;
 CC Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFPSLTKVNVKVPKPIGENNENEOSSRRNEEGSHSPSNQSOQTAAEENKGEKSLTKSTPV 60
 DB 1 MFPSLTKVNVKVPKPIGENNENEOSSRRNEEGSHSPSNQSOQTAAEENKGEKSLTKSTPV 60
 QY 61 TSEBPHITIQDKLSKKNSSGDLTTNPDPQNAEAETGTVPPEQKEMDPGKEGPNSPONKPPA 120
 DB 61 TSEBPHITIQDKLSKKNSSGDLTTNPDPQNAEAETGTVPPEQKEMDPGKEGPNSPONKPPA 120
 QY 121 APVINEYADAQHLNVLKRMORTALYKKLVGDDLSSEASPOAKPTAVPVKESDDKP 180
 DB 121 APVINEYADAQHLNVLKRMORTALYKKLVGDDLSSEASPOAKPTAVPVKESDDKP 180
 QY 181 TEHYRLLRFKVKMKPLTEYLKRIKLPSIDSYTDRLYLLMLLVTLAYNNWCWFIPLRL 240
 DB 181 TEHYRLLRFKVKMKPLTEYLKRIKLPSIDSYTDRLYLLMLLVTLAYNNWCWFIPLRL 240
 QY 241 VPPYQTADNIHYWLIADIICDIIYLYDMLFQPRLOQFVRGGDIIVDSNELRKHYRTSTKF 300
 DB 241 VPPYQTADNIHYWLIADIICDIIYLYDMLFQPRLOQFVRGGDIIVDSNELRKHYRTSTKF 300
 QY 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAVIYVIRTTGYL 360
 DB 301 QLDVASIIPFDICYLFFGFNPMFRANRMLKYTSFFEFNHHLESIMDKAVIYVIRTTGYL 360
 QY 361 LFIILHINACVYVWASNYEGIGTRVWYDGEYELRCYVWAVRTLTITIGLPEPOTLFEI 420
 DB 361 LFIILHINACVYVWASNYEGIGTRVWYDGEYELRCYVWAVRTLTITIGLPEPOTLFEI 420
 QY 421 VFQLLNFFSGVVFVSSLIQGMRDVITGAATANQNYFRACMDDTIAYNNYSIIPKLQKVR 480
 DB 421 VFQLLNFFSGVVFVSSLIQGMRDVITGAATANQNYFRACMDDTIAYNNYSIIPKLQKVR 480
 QY 481 TWVEYTWDSQRMLEDSDLLKTLPTTVQALATDVNFSIISKVDLPKGDOTMIYDMLLRL 540
 DB 481 TWVEYTWDSQRMLEDSDLLKTLPTTVQALATDVNFSIISKVDLPKGDOTMIYDMLLRL 540
 QY 541 KSVLYLPDGFVCKGEGIKEMWIIKHGEVQVLGGPDGTVKLVTLKAGSVFGESISLLAAGG 600
 DB 541 KSVLYLPDGFVCKGEGIKEMWIIKHGEVQVLGGPDGTVKLVTLKAGSVFGESISLLAAGG 600
 QY 601 GNRRTANVVAHGFANLLTLDKKTLOEILVHVPDSEIRIIMKKARVLLKOKAKTAEATPPRK 660
 DB 601 GNRRTANVVAHGFANLLTLDKKTLOEILVHVPDSEIRIIMKKARVLLKOKAKTAEATPPRK 660
 QY 661 DLALLFPKKEETPKLFTLLGGTGKASLARLLKLKREAAOKKENSEGEGEGKENEKQ 720
 DB 661 DLALLFPKKEETPKLFTLLGGTGKASLARLLKLKREAAOKKENSEGEGEGKENEKQ 720
 QY 721 KENEDKQENEDKGENEDKKGREPEBKPLDRPECTASPIAVEEPEHPSVRRVTLPRGTS 780
 DB 721 KENEDKQENEDKGENEDKKGREPEBKPLDRPECTASPIAVEEPEHPSVRRVTLPRGTS 780
 QY 781 ROSLIISMAPSAGEGEEVLTIEVKEKAKQ 809
 DB 781 ROSLIISMAPSAGEGEEVLTIEVKEKAKQ 809
 RESULT 2
 CNGB3 CANPA
 ID CNGB3 CANPA STANDARD; PRT; 782 AA.
 AC Q8MJD7;
 DT 29-MAR-2004 (Rel. 43, Created)
 DT 29-MAR-2004 (Rel. 43, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Cyclic-nucleotide-gated cation channel beta 3 (CNG channel beta 3)
 DE (Cyclic nucleotide gated channel beta 3) (Cone photoreceptor cGMP-
 DE gated channel beta subunit) (Cyclic nucleotide-gated cation channel
 DE modulatory subunit).
 GN Name=CNGB3;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.

NCBI_TaxID=9615;
[1]
RN NUCLEOTIDE SEQUENCE [MRNA], AND VARIANT CD ASN-262.
RX PubMed=12140185; DOI=10.1093/hmg/11.16.1823;
RA Sidjanin D.J., Lowe J.K., McElwee J.L., Milne B.S., Phippen T.M.,
RA Sargan D.R., Aguirre G.D., Acland G.M., Ostrander E.A.;
RT "Canine CNGB3 mutations establish cone degeneration as orthologous to
RL the human achromatopsia locus ACHM3.";
RL Hum. Mol. Genet. 11:1823-1833(2002).
CC -1- FUNCTION: Visual signal transduction is mediated by a G-protein
CC coupled cascade using cGMP as second messenger. This protein can
CC be activated by cGMP which leads to an opening of the cation
CC channel and thereby causing a depolarization of rod
CC photoreceptors. Induced a flickering channel gating, weakened the
CC outward rectification in the presence of extracellular calcium,
CC increased sensitivity for L-cis diltiazem and enhanced the cAMP
CC efficacy of the channel when coexpressed with CNGB3. Essential for
CC the generation of light-evoked electrical responses in the red-,
CC green- and blue sensitive cones (By similarity).
CC -1- SUBUNIT: Heterooligomeric complex with CNGB3 (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- DISEASE: Defects in CNGB3 are a cause of cone degeneration (cd).
CC Cd is characterized by day-blindness and absence of retinal cone
CC function. This autosomal recessive disorder occurs naturally in
CC the Alaskan Malamute and German Shorthaired Pointer breeds.
CC -1- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -1- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AF490511; AAM89224.1; -; mRNA.
DR Ensembl; ENSCAFG0000008906; Canis familiaris.
DR InterPro; IPR000595; CNMP_bd.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00520; CNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; CNMP; 1.
DR PROSITE; PS00888; CNMP_BINDING_1; 1.
DR PROSITE; PS00889; CNMP_BINDING_2; 1.
DR PROSITE; PS50042; CNMP_BINDING_3; 1.
KW cGMP; cGMP-binding; Disease mutation; Ion transport; Ionic channel;
KW Multigene family; Nucleotide-binding; Sensory transduction;
KW Transmembrane; Transport; Vision.
FT TOPO_DOM 1 211 Cytoplasmic (Potential).
FT TRANSMEM 212 232 H1 (Potential).
FT TOPO_DOM 233 245 Extracellular (Potential).
FT TRANSMEM 246 266 H2 (Potential).
FT TOPO_DOM 267 297 Cytoplasmic (Potential).
FT TRANSMEM 298 318 H3 (Potential).
FT TOPO_DOM 319 412 Extracellular (Potential).
FT TRANSMEM 413 433 H4 (Potential).
FT TOPO_DOM 434 493 Cytoplasmic (Potential).
FT TRANSMEM 494 514 H5 (Potential).
FT TOPO_DOM 515 572 Extracellular (Potential).
FT TRANSMEM 573 593 H6 (Potential).
FT TOPO_DOM 594 782 Cytoplasmic (Potential).
FT NP_BIND 527 671 cGMP (By similarity).
FT BINDING 587 587 cGMP (By similarity).
FT BINDING 599 599 cGMP (By similarity).
FT VARIANT 262 262 D -> N (in cd; in a German Shorthaired Pointer).
SQ SEQUENCE 782 AA; 89424 MW; 7139EF3B86268A79 CRC64;
Query Match 75.11%; Score 3181.5; DB 1; Length 782;
Best Local Similarity 76.2%; Pred. No. 3.3e-177;
Matches 618; Conservative 57; Mismatches 105; Indels 31; Gaps 5;

OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE, FUNCTION, SUBUNIT, AND TISSUE SPECIFICITY.
 RC STRAIN=C57BL/6; TISSUE=Retina;
 RA MEDLINE=20130348; PubMed=10662822;
 RX Gerstner A., Zong X., Hofmann F., Biel M.;
 RT "Molecular cloning and functional characterization of a new modulatory
 cylic nucleotide-gated channel subunit from mouse retina.";
 RL J. Neurosci. 20:1324-1332(2000).
 CC -!- FUNCTION: Visual signal transduction is mediated by a G-protein
 coupled cascade using cGMP as second messenger. This protein can
 be activated by cGMP which leads to an opening of the cation
 channel and thereby causing a depolarization of rod
 photoreceptors. Essential for the generation of light-evoked
 electrical responses in the red-, green- and blue sensitive cones
 (By similarity). Induced a flickering channel gating, weakened the
 outward rectification in the presence of extracellular calcium.
 CC increased sensitivity for L-cis diltiazem and enhanced the cAMP
 efficacy of the channel when coexpressed with CNGB3.
 CC -!- SUBUNIT: Heterooligomeric complex with CNGB3.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- TISSUE SPECIFICITY: Small subset of retinal photoreceptor cells and
 testis.
 CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
 (TC 1.A.1.5) family.
 CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
 CC -----
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 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC -----
 CC EMBL; AJ243572; CAB71152.1; -; mRNA.
 DR Ensembl; ENSMUSG0000056494; Mus musculus.
 DR MGI; MGI:1323562; Cnbg3.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR GO; GO:0005886; C:plasma membrane; IC.
 DR GO; GO:0030553; F:3',5'-cGMP binding; IC.
 DR GO; GO:0005223; F:intracellular cGMP activated cation channel. . .; IPI.
 DR GO; GO:0009187; P:cyclic nucleotide metabolism; IC.
 DR InterPro; IPR000595; cGMP bd.
 DR InterPro; IPR005821; Ion_trans.
 DR InterPro; IPR001622; K-channel_pore.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR Pfam; PF00520; Ion_trans; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; 1.
 DR PROSITE; PS00889; cNMP_BINDING_2; 1.
 DR PROSITE; PS00942; cNMP_BINDING_3; 1.
 KW cGMP; cGMP-binding; Glycoprotein; Ion transport; Ionic channel;
 KW Multigene family; Nucleotide-binding; Sensory transduction;
 KW Transmembrane; Transport; Vision.
 FT TOPO_DOM 1 209 Cytoplasmic (Potential).
 FT TRANSMEM 210 230 H1 (Potential).
 FT TOPO_DOM 231 242 Extracellular (Potential).
 FT TRANSMEM 243 263 H2 (Potential).
 FT TOPO_DOM 264 294 Cytoplasmic (Potential).
 FT TRANSMEM 295 315 H3 (Potential).
 FT TOPO_DOM 316 351 Extracellular (Potential).
 FT TRANSMEM 352 372 H4 (Potential).
 FT TOPO_DOM 373 409 Cytoplasmic (Potential).
 FT TRANSMEM 410 430 H5 (Potential).
 FT TOPO_DOM 431 568 Extracellular (Potential).
 FT TRANSMEM 569 589 H6 (Potential).
 FT TOPO_DOM 590 694 Cytoplasmic (Potential).
 FT NP_BIND 524 668 cGMP (By similarity).
 FT BINDING 584 594 cGMP (By similarity).
 FT BINDING 596 596 cGMP (By similarity).
 FT CARBOHYD 507 507 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 694 AA; 79722 MW; 0B9F9CF3B180DA82 CRC64;

Query Match

Best Local Similarity 68.7%; Pred. No. 2.3e-138;
 Matches 485; Conservative 92; Mismatches 113; Indels 16; Gaps 7;
 QY 1 MFKSLLT-KVNVKPKPGENNENESQRRNEEGSHP--SNOSQOTTAQEEKNKGEKSLKTKS 57
 DB 1 MKSLLTVPKKNVPM-----EGRMEKKLCPNLSSLSQPTIAQGNQSEKEPLRSR- 50
 QY 58 TPVTSEEPHTNTQDKLSKKNSSGDLTTPNPDQNAAEPTGTVPPEQKEMDPKGEKSPNQK 117
 DB 51 TPITFEKSHK-EDNSTGENSLRDPNPDPECAELTRTMAEMEKTRTKGERPVSFKTK 109
 QY 118 PPAAPVINEYADAQLHNLVKMRQRTALYKKKLKLVGEG-LSPEASPTAKPTAVIPVKIS 176
 DB 110 VLETSIINEYTDALHNLVRRMRRTALYKKTLTTEENFPEVEASSOTAMSTN1SPKQFN 69
 QY 177 DDKPTHEHYVRLWPKVKMPLETKR1KLPNSIDSYTDLRYLLWLLLVTLAYNWCW1 146
 DB 170 NSKLKEH-QDTFSFAPQRPVKEHURMLPRSIDSYTDRVYLLWLLLVTLAYNWCW1 228
 QY 237 PLRLVFPYQTADNIHYLIADIICDIIYLYDMLFIQPRLQFVRRGGDIIVDSNELKHYRT 296
 DB 229 PVRLVFPQTPDNKNYWIITDVCIIYLCIDILLQPRLQFVRRGGDIIVDSNELKRYRS 288
 QY 297 STKFQDVAASIIIPDICYLFFGPNMFRANRMLKYTSFFEFNNHLESIMDKAYIYRVIRT 356
 DB 289 STKFRMDVASLLPPEVLYIFFGVNPIFRANRILKYTSFFEFNNHLESIMDKAYVYRVIRT 148
 QY 357 TGYLLFLIHINACVYVWASNYEGIGTTRWVDGEGEYLRVYVAVRTLTITIGGLPEPOT 416
 DB 349 TGYLLFLIHINACVYVWASDYEGIGTRWVYNGEKNYLRCPYVAVRTLTITIGGLPEPOT 408
 QY 417 LFEIVQLLNFFSGVVFVSSLLIGQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKLVO 476
 DB 409 SFEIVFQFLNFFSGVVFVSSLLIGQMRDVI GAATANQNYFQACMDHI IAYMNNYSIPQSVQ 468
 QY 477 KRVRTWYETWDSQRMDESLLKTLPTTVQALAIQVNFNFIISKVDLPFKGCDTOMIDM 536
 DB 469 YRVRTWLEYTWNQSRLDESLLNLENLPTAMOLSIADLINFISIDKVELFKGCDTOMIDL 528
 QY 537 LLRLKSLVLYPGDFVCKKGEIGKEMYYIKHGEVQVLGGPDGPKVLVTLKAGSVFGEISLL 596
 DB 529 LLRLKSTIYLPDGFVCKKGEIGKEMYYIKHGEVQVLGGPDGQAVLVTLKAGSVFGEISLL 588
 QY 597 AAGGNNRRTANVAHGFANLLTLDKKTQLQELIVHYPSERILMKKARVLLKOKAKTAEAT 656
 DB 589 AKGGNNRRTADVVAHGFANLLTLDKKTQLQELIVHYPSERILMKKAKILLKOKGKTQAI 648
 QY 657 PPRKDLALLFPKKEPKLFTLLCGTCKASLARIALLKREOAAOK 702
 DB 649 PARPGPAFLFPKKEPKLFTLLCGTCKASLARIALLKREOAAOK 694
 RESULT 4
 Q80XL8 MOUSE
 ID Q80XL8_MOUSE PRELIMINARY; PRT; 866 AA.
 AC Q80XL8;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Cnbg1b protein (Fragment).
 GN Name=Cnbg1b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathu;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

[illegible]


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QY 441 MRDVTGAATANQNYFRACMDDTIANNYSIPKLQKRVRTWYETWDSQRLMDESDLLK 500
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
537 MRDVVGAATAGQTYRSCNDSTVKYMNFKIPKSVQNRVKTWYETWHSQGLMDESELMV 596
QY 501 TLPTTVQALALADVNFSIISKVDLFGKCDTOMYDMLLRLKSVLYLPDGFVCKKGEIGKE 560
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
597 QLPDKMRLDLADVNINYSKVALFGCDRQIFDMLKELRSVVYLPNDYVCKKGEIGRE 656
QY 561 MYIIKHGEVQVLGGPDGTVLVTLKAGSVFGISILAAAGGNNRRTANVAHGFANLLTLD 620
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
657 MYIIQAGVQVVLGGPDGKSVLTLKAGSVFGISILAVGGNNRRTANVAHGFANLLTLD 716
QY 621 KKTLEILVHYVPSERILMKKARVLKQAKTAETPPRKDLALLPFPKEETPKLFTKLL 680
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
717 KKDLEILVHYVPSOKLLRKARRMLRSNNK-----PKEEKSVLLIPPRAGTPKLFNAAL 771
QY 681 GGTGKAS-----LARKLLKREQAQKKNSEGGEEGKENEDKQK 728
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
772 AMTGKMGKGKAGGKLAHLARLAKELAALEAAKHEEL---VEQAKSQDVKGEGSAAP 828
QY 729 ENEDKGKE-NEDKDKGREPEEKPLDRPECTASPIAV-----BEEPHSVRRTVLP 776
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
829 DQHTHPKEAATUPPAPRTPEPP-GSPSSPPASLGSCGEGEPAEPEHSVR-----882
QY 777 RQTSRQSLIISMAPSAEGGEVLTIEVKKAKQ 809
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
883 -----ICMSPGPEGEGILSVKMPEREE 906

RESULT 8
Q9UMG2_HUMAN
ID Q9UMG2_HUMAN PRELIMINARY; PRT; 1251 AA.
AC Q9UMG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE cGMP-gated cation channel beta subunit.
GN Name=CNGB1; Synonyms=CNGC2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=96070429; PubMed=7590744;
RA Ardell M.D., Makhija A.K., Oliveira L., Miniou P.,
RA Viegas-Pequignot E., Pittler S.J.;
RT "cDNA, gene structure, and chromosomal localization of human GARI
RT (CNGC3L), a homolog of the third subunit of bovine photoreceptor cGMP-
RT gated channel.";
RL Genomics 28:32-38(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Retina;
RX MEDLINE=96338110; PubMed=8766832; DOI=10.1016/0014-5793(96)00588-1;
RA Ardell M.D., Aragon I., Oliveira L., Porche G.E., Burke E.,
RA Pittler S.J.;
RT "The beta subunit of human rod photoreceptor cGMP-gated cation channel
RT is generated from a complex transcription unit.";
RL FEBS Lett. 389:213-218(1996).
DR EMBL; U58837; AAB363387.1; -, mRNA.
DR PIR; S69275; S69275.
DR HSP; O88703; I043.
DR Ensembl; ENSG00000070729; Homo sapiens.
DR HGNC; HGNC:12151; CNGB1.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0030553; F:3',5'-cGMP binding; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0000166; F:nucleotide binding; IEA.

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DR GO; GO:0005267; F:potassium channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR GO; GO:0006813; P:potassium ion transport; IEA.
DR GO; GO:0007601; P:visual perception; IEA.
DR InterPro; IPR000595; cNMP_binding.
DR InterPro; IPR005821; Ion_trans.
DR InterPro; IPR001622; K-channel_pore.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF00520; Ion_trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00888; cNMP_BINDING_1; UNKNOWN 1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
SQ SEQUENCE 1251 AA; 139604 MW; 4701C53DB13C9055 CRC64;

Query Match 46.0%; Score 1949; DB 2; Length 1251;
Best Local Similarity 46.2%; Pred.No. 5.5e-105;
Matches 403; Conservative 122; Mismatches 238; Indels 110; Gaps 18;

QY 14 IGNNENEQSSRRNEEGSHPSNQSOQTAAQE--ENKGE---EKSLTKSTPTVTSSEPHTN 68
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
409 VGEEAKKEAEKAEKEAEVEAEAEKEPDWAETKEEPEAEAEASSGVPATKQHPVQ 468
QY 69 IQDK-----LSKNSSGDLTTNPDQNAAEPTCTVPEQKEMDPGKEGPN----- 112
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
469 VEDTDADSCPLMAEENPPS--TVLPPSPAKSDTLIVPSSASGTHRKKLPSDEDAEELK 526
QY 113 --SPONKP-----PAAP-----VINEYADAOLHNLVKMRORTALY 146
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
527 ALSPAESPVAWSDPTTPKDTGQDRAASTASTNSAIIND---RLQELVLKFKERTKV 582
QY 147 KKKLVEGDLS---SPEASQPTAKPTAVPPVKESDDKPT--EHYVRLILFWKVKMPLTEY 200
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
583 KEKLIDPDVTSDEESPSPAKKAPAPDTKPAEAPVEEHEHYCDMLKCKFKHPWKY 642
QY 201 LKRIKPNISDYDRLVLLMLLVLTLAYNNCWPIPLURLVPFQOTADNIHWLIADII 760
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
643 ---QFQSIDPLTNLMVLMVLFVVMANNWNCNLIPIVRWAPPYQTPONIIHMLLMDVLK 698
QY 261 DIILYDMLFIQPLQFVRGGDIIVDSNELRKHRTSTKFDLDVASIIPFDICYLFFGPN 320
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
699 DLIVFLDTVFTQLQFVRGGDITDKKDMRNLYKRRFKMDLSLPLDPLFLYLUKGVN 758
QY 321 PMFRANRLKYTSFEFFNHHLESIMDKAYIRVIRTTCYLLFILHINACVYVWASNYEGI 380
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
759 PLLRLPRCLKYMAPEFNPRLSILSKAYVVRVIRTAYLLYSLHNSCLYVWASAYQGI 818
QY 381 GTTRWYDGEVRLCYVWAVRILITIGLPPEOTLPEIVFOLLNFTSGVPVFSLLIG 440
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
819 GSTHWYDGVGNSVIRCYFAVKTITIGLPDPKTLFEIVFOLLNYFTGVFAFVMIQ 878
QY 441 MRDVI GAATANQNYFRACMDDTIAMNNYSIPKLQKRVRTWYETWDSQRLMDESDLLK 500
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
879 MRDVVGAATAGQTYRSCNDSTVKYMNFKIPKSVQNRVKTWYETWHSQGLMDESELMV 938
QY 501 TLPTTVQALALADVNFSIISKVDLFGKCDTOMYDMLLRLKSVLYLPDGFVCKKGEIGKE 560
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
939 QLPDKMRLDLADVNINYSKVALFGCDRQIFDMLKELRSVVYLPNDYVCKKGEIGRE 998
QY 561 MYIIKHGEVQVLGGPDGKSVLTLKAGSVFGISILAAAGGNNRRTANVAHGFANLLTLD 620
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
999 MYIIQAGVQVVLGGPDGKSVLTLKAGSVFGISILAVGGNNRRTANVAHGFANLLTLD 1058
QY 621 KKTLEILVHYVPSERILMKKARVLKQAKTAETPKRDLALLPFPKEETPKLFTKLL 680
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1059 KKDLEILVHYVPSOKLLRKARRMLRSNNK-----PKEEKSVLLIPPRAGTPKLFNAAL 1113
QY 681 GGTGKAS-----LARKLLKREQAQKKNSEGGEEGKENEDKQK 728
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1114 AMTGKMGKGKAGGKLAHLARLAKELAALEAAKHEEL---VEQAKSQDVKGEGSAAP 1170
QY 729 ENEDKGKE-NEDKDKGREPEEKPLDRPECTASPIAV-----BEEPHSVRRTVLP 776
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 387 YDGEYNEILRCYVAVRTLTITIGLPEPOTLFEIVFOLLNFFSGVFVFSLSLQMRDVTG 446
Db 493 YDGVGNSYRCYVAVRTLTITIGLPEPOTLFEIVFOLLNFFSGVFVFSLSLQMRDVTG 552
QY 447 AATANQYPRACNDTIIAYNNYSIPKLVQKRVTHYVETWDSORMLDESLLKTLPTTV 506
Db 553 AATAGQTYRSCMDSTVKYWNFYKIPRSVQNRVKTWYETWHSQGMDESLVQVLPDKM 612
QY 507 QLALAIADVNFISIISKVLDLFGKCDTOMIYDMLRLKSVLYLPGDFVCKGGEIGKEMIIKH 566
Db 613 RLDAIDVNVYSIVSKVALFGCDROMIFDMLKRLSVVLYPNDYVCKGGEIGREMYIIOA 672
QY 567 GEVQVLGGPDGKVLVTLKAGSVFGEISILAAAGGNRRRTANVVAHFANLLTLDKKTLOE 626
Db 673 GQVQVLGGPDGKSVLTLKAGSVFGEISILAAAGGNRRRTANVVAHFANLLTLDKKTLOE 732
QY 627 ILVHYPDSEIRILMKARVLLKOKAKTAEATPPRKDLALLFPKKEETPKLFTLLGGTGKA 686
Db 733 ILVHYPESQKLRLKARMLRNKK-----PKEKSVLILPPRAGTPKLFNAALAAAGKM 786
QY 687 SL-----ARLLKLKREQAQKKNSESGEENEDKOKENEDKOKENEDKG 734
Db 787 GAKGGRGRLALLRLKELAALEAAARQOOL-----LEQAQKSEDAAGVEE-----G 834
QY 735 KENEDKDKGPEPEKPLDRPECTA-----SPIAVEEPPHSVRRTVLP 776
Db 835 SASPEQPPRPEPAPEAPEPTAPEPLAPEAPEAPAPSSPPASQERPEGDKDAARP 894
QY 777 RGTSRQSLIISMAPSAEGGEVLTIEVKEKAKQ 809
Db 895 ---EEHPVRIHVTLGPDPSQILLVEVPEKQEE 924

RESULT 12
O77660_BOVIN PRELIMINARY; PRT; 952 AA.
ID AC O77660;
DT 01-NOV-1998 (T-EMBLrel. 08, Created)
DT 01-NOV-1998 (T-EMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Cyclic nucleotide-gated channel beta subunit 1e.
GN Name=CNCbeta;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98345361; PubMed=9679145; DOI=10.1083/jcb.142.2.473;
RA Wiesner B., Weiner J., Middendorff R., Hagen V., Kaupp U.B.,
RA Weyand I.;
RT "Cyclic nucleotide-gated channels on the flagellum control Ca2+ entry
into sperm.";
RL J. Cell Biol. 142:473-484(1998).
DR EMBL; AF074014; AAC26129.1; -, mRNA.
DR HSSP; O88703; 1043.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005216; F:ion channel activity; IEA.
DR GO; GO:0006811; P:ion transport; IEA.
DR InterPro; IPR00595; cNMP binding.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP binding; 1.
DR Pfam; PF00520; Ion_Trans; 1.
DR SMART; SM00100; cNMP; 1.
DR PROSITE; PS00886; cNMP_BINDING_1; UNKNOWN_1.
DR PROSITE; PS00889; cNMP_BINDING_2; 1.
DR PROSITE; PS00442; cNMP_BINDING_3; 1.
DR PROSITE; PS00442; cNMP_BINDING_4; 1.
SQ SEQUENCE 952 AA; 105913 MW; D43F8BD127F7F052 CRC64;

Query Match 45.3%; Score 1920; DB 2; Length 952;
Best Local Similarity 45.9%; Pred. No. 1.9e-103;
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Matches 401; Conservative 118; Mismatches 242; Indels 112; Gaps 17;
QY 15 GENNESSRRNEEGSHPSNQSOQTAAQENKNGBEKSLTKSTPTVTSEPTNIQDK-- 72
Db 90 GAQAQGEVGAQEQDQGVGA-QDQSTSHQEL--BEALADSSGVPAATEHPHQLQVEDADA 146
QY 73 -----LSKNSSGDLTTNPDPQNAAEPTGCTVP-----EOKEMDPCK 108
Db 147 DSRPLIAEENPPSPVOLPLSP--AKSDTLAVPGSATGSLRKRLPSODDDAEELKMLSPAA 204
QY 109 -----EGNSPNKPPA-----APVINEYADAQHLNLVKRMORTALYKKKLVE 152
Db 205 SPVWMSDPTSFGQDDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQDQD 260
QY 153 GDLS-----SPEASPTAKPTAVPPVK--ESDDKPTHEYRLLLFWFKVKMPLTEYLKRIKL 206
Db 261 PDVTSDEESPKEKSPAKAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP 316
QY 207 PHSIDSYDRLVLLMLLLVTLAYNNCWFIPLRLVFPYOTADNIHYMLADIICDIIYLY 266
Db 317 POSIDPLTLMLYILMLFFVLLANNWCWLIPLVRVAPPYOTPDNIHLMLMDVYLCDDIYLL 376
QY 267 DMLFTQPLQFVRGGDIIIVDSNELKGYRTSTKFDQDVASIIIPFDICYLFFGFNPMFRAN 326
Db 377 DITVFQMRLOFVRGGDIIIDKEMRNYYKVSQRFKMDMLCLPLDLLLYLFKGVNPLRLP 436
QY 327 RMLKYTFPFNNHLESIMDKAYIYRVIRTTGVLFLPHINACVYVWASNYEGIGTRVW 386
Db 437 RCLKYMAFPEFNNLESILSKAYVYRVIRTTAYLLYSLHNSCLYVWASNYEGIGSTHW 496
QY 387 YDGEYNEILRCYVAVRTLTITIGLPEPOTLFEIVFOLLNFFSGVFVFSLSLQMRDVTG 446
Db 497 YDGVGNSYRCYVAVRTLTITIGLPEPOTLFEIVFOLLNFFSGVFVFSLSLQMRDVTG 556
QY 447 AATANQYPRACNDTIIAYNNYSIPKLVQKRVTHYVETWDSORMLDESLLKTLPTTV 506
Db 557 AATAGQTYRSCMDSTVKYWNFYKIPRSVQNRVKTWYETWHSQGMDESLVQVLPDKM 616
QY 507 QLALAIADVNFISIISKVLDLFGKCDTOMIYDMLRLKSVLYLPGDFVCKGGEIGKEMIIKH 566
Db 617 RLDAIDVNVYSIVSKVALFGCDROMIFDMLKRLSVVLYPNDYVCKGGEIGREMYIIOA 676
QY 567 GEVQVLGGPDGKVLVTLKAGSVFGEISILAAAGGNRRRTANVVAHFANLLTLDKKTLOE 626
Db 677 GQVQVLGGPDGKSVLTLKAGSVFGEISILAAAGGNRRRTANVVAHFANLLTLDKKTLOE 736
QY 627 ILVHYPDSEIRILMKARVLLKOKAKTAEATPPRKDLALLFPKKEETPKLFTLLGGTGKA 686
Db 737 ILVHYPESQKLRLKARMLRNKK-----PKEKSVLILPPRAGTPKLFNAALAAAGKM 790
QY 687 SL-----ARLLKLKREQAQKKNSESGEENEDKOKENEDKOKENEDKG 734
Db 791 GAKGGRGRLALLRLKELAALEAAARQOOL-----LEQAQKSEDAAGVEE-----G 838
QY 735 KENEDKDKGPEPEKPLDRPECTA-----SPIAVEEPPHSVRRTVLP 776
Db 839 SASPEQPPRPEPAPEAPEPTAPEPLAPEAPEAPAPSSPPASQERPEGDKDAARP 898
QY 777 RGTSRQSLIISMAPSAEGGEVLTIEVKEKAKQ 809
Db 899 ---EEHPVRIHVTLGPDPSQILLVEVPEKQEE 928

RESULT 13
CNCB1_BOVIN STANDARD; PRT; 1394 AA.
ID AC Q28181; Q03861; Q28082;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE 240 kDa protein of rod photoreceptor CNG-channel (Contains: Glutamic
DE acid-rich protein (GARP); Cyclic nucleotide-gated cation channel 4
DE (CNG channel 4) (CNG-4) (Cyclic nucleotide-gated cation channel
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DE modulatory subunit)].
GN Name=CNGB1; Synonyms=CNGC4;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RX MEDLINE=96009859; PubMed=7546742; DOI=10.1016/0896-6273(95)90151-5;
RA Koerschen H.G., Iilling M., Seifert R., Seeti F., Williams A.,
RA Gotzes S., Colville C., Mueller F., Dose A., Godde M., Molday L.,
RA Kaupp U.B., Molday R.S.;
RT "A 240 kDa protein represents the complete beta subunit of the cyclic
RT nucleotide-gated channel from rod photoreceptor.";
RL Neuron 15:627-636(1995).
RN [2]
RP NUCLEOTIDE SEQUENCE OF 454-1394 (ISOFORMS CNG4C; CNG4D AND CNG4E).
RC TISSUE=retina;
RX MEDLINE=96198098; PubMed=8626431; DOI=10.1074/jbc.271.11.6349;
RA Biel M., Zong X., Ludwig A., Sautter A., Hofmann F.;
RT "Molecular cloning and expression of the modulatory subunit of the
RT cyclic nucleotide-gated cation channel.";
RL J. Biol. Chem. 271:6349-6355(1996).
RN [3]
RP NUCLEOTIDE SEQUENCE OF 1-590.
RC TISSUE=Retina;
RX PubMed=2014230;
RA Sugimoto Y., Yatsunami K., Tsujimoto M., Khorana H.G., Ichikawa A.;
RT "The amino acid sequence of a glutamic acid-rich protein from bovine
RT retina as deduced from the cDNA sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3116-3119(1991).
CC -!- SUBUNIT: Forms functional heterooligomeric channels with CNG3.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Comment-Isoform CNG4D is the most frequent isoform
CC (CNG4D; CNG4E = 20:21) in testis;
CC Name=CNG4C;
CC IsoId=Q28181-1; Sequence=Displayed;
CC Name=CNG4D;
CC IsoId=Q28181-2; Sequence=VSP_001109;
CC Name=CNG4E;
CC IsoId=Q28181-3; Sequence=VSP_001108;
CC -!- TISSUE SPECIFICITY: Retina, testis, kidney, heart and brain.
CC -!- SIMILARITY: Belongs to the cyclic nucleotide-gated cation channel
CC (TC 1.A.1.5) family.
CC -!- SIMILARITY: Contains 1 cyclic nucleotide-binding domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; X89626; CAA61769.1; -; mRNA.
DR EMBL; X94707; CAA64367.1; -; mRNA.
DR EMBL; M61185; AAA30536.1; -; mRNA.
DR PIR; A40437; A40437.
DR InterPro; IPR000595; CNGP bd.
DR InterPro; IPR005821; Ion Trans.
DR Pfam; PF00027; cNMP_binding; 1.
DR Pfam; PF05520; Ion_trans; 1.
DR PROSITE; PS00888; CNGP_BINDING_1; 1.
DR PROSITE; PS00889; CNGP_BINDING_2; 1.
DR PROSITE; PS00442; CNGP_BINDING_3; 1.
KW Alternative splicing; CAMP; cAMP-binding; Direct protein sequencing;
KW Glycoprotein; Ion transport; Ionic channel; Multigene family;
KW Nucleotide-binding; Transmembrane; Transport.
FT CHAIN 1 590 Glutamic acid-rich protein.
FT CHAIN 454 1394 Cyclic-nucleotide-gated cation channel 4.
FT TOPO_DOM 1 770 Cytoplasmic (Potential).
FT TRANSMEM 771 789 HI (Potential).

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FT TOPO_DOM 790 803 Extracellular (Potential).
FT TRANSMEM 804 822 H2 (Potential).
FT TOPO_DOM 823 847 Cytoplasmic (Potential).
FT TRANSMEM 848 867 H3 (Potential).
FT TOPO_DOM 868 904 Extracellular (Potential).
FT TRANSMEM 905 927 H4 (Potential).
FT TOPO_DOM 928 971 Cytoplasmic (Potential).
FT TRANSMEM 972 991 H5 (Potential).
FT TOPO_DOM 992 1075 Extracellular (Potential).
FT TRANSMEM 1076 1096 H6 (Potential).
FT TOPO_DOM 1097 1222 CAMP (By similarity).
FT BINDING 1144 1156 CAMP (Potential).
FT BINDING 1156 1156 CAMP (Potential).
FT CARBOHYD 1067 1067 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 515 532 Missing (in isoform CNG4E).
FT VARSPLIC 522 530 /FTid=VSP_001108.
FT VARSPLIC 530 530 Missing (in isoform CNG4D).
FT CONFLICT 341 341 /FTid=VSP_001109.
FT CONFLICT 454 465 K -> E (in Ref. 3).
FT CONFLICT 482 482 REEEDDEEED -> MRAGQKGR (in Ref. 2).
FT CONFLICT 499 499 R -> Q (in Ref. 2 and 3).
FT CONFLICT 572 590 A -> T (in Ref. 3).
FT CONFLICT 572 590 VPATEEHEPELOVEDADADS -> GSFQMSPFALORCEALAK
FT CONFLICT 1283 1283 R (in Ref. 3).
FT CONFLICT 1289 1289 S -> A (in Ref. 2).
FT CONFLICT 1336 1336 R -> A (in Ref. 2).
FT CONFLICT 1338 1338 D -> E (in Ref. 2).
FT CONFLICT 1394 AA; 155065 MW; EE6DA59BE3744A7 CRC64;
SQ SEQUENCE 1394 AA; 155065 MW; EE6DA59BE3744A7 CRC64;

Query Match 45.3%; Score 1920; DB 1; Length 1394;
Best Local Similarity 45.9%; Pred. No. 3.2e-103;
Matches 401; Conservative 118; Mismatches 24; Indels 112; Gaps 17.

QY 15 GENNEOSSRRNEEGSHPSNQSOQTAAEQENKGEKSLKTKSTPVTSEEPHTNODK 72
DB 532 GAQAQGEVGGABQDQGVGA-QDQSTSHQELQ--EEALADSSGVPAEHEPELOVEDADA 588
QY 73 -----LSKNSGDLTNPDPQNAAEPTGTVP-----EOKEMDPCK 108
DB 589 DSRPLIAEENPPSPVQLPLSP--AKSDTLAVPGSATGSLRKLPSQDDEAEELKMLSPA 646
QY 109 -----EGNPSQNKPPA-----APVNEYADAQLHNLVKRMORTALYKKKLVE 152
DB 647 SPVVAWSPTSPQGTDDQDRATSTASQNSAIND---RLQELVKLFKERTKVKELID 702
QY 153 GDLS-----SPASQTAKTAVPPVK--ESDDKPTHEYRLLLWFKVKMPLTEYLKRIKL 206
DB 703 PDVTSDEESPKSPAKKAPAEVPAEAGQVEEHYCEMLCKFKRPPWKY----QF 758
QY 207 PMSIDSYTRLYLLMLLVLTAYNNWCFILRLVFPYQTDADNIHYWLIADIIIDIIYLY 266
DB 759 PQSIDPLTNLMYLLWLFVVLAWNNCWLI PVRAWFPYQTPDNIHLWLMMDYLCCLLYLL 818
QY 267 DMLFTQPRQLQVRGGDIIVDSNELRKHRYTSTKFDQDVASIIIPFDICYLFFGFNPMFRAN 126
DB 819 DITVFQMLQLQVRGGDIITDKKEMRNNVKVSQRFKMDMLCLLPLDLLYLKFGVNPLLRLP 878
QY 327 RMLKYSFFENHHLESMDKAYIYRVTRTGYLLFILHINACVYVWASNYEGIGTTRWV 386
DB 879 RCLKYMAFFENNRLESLSKAYVYVIRTTAYLLYSLHNSCLYVWASAYEGLGSTHWV 938
QY 387 YDGEQNEVLCYVAVRLLTIIGGLPEPQTLFEIVFQLNFFSGVVFSSLIQMRDVIG 446
DB 939 YDGVGNSVIRCYVAVKTLTIIGGLPDRTLFEIVFQGLNYFTGVFAFSVMIQMRDVVG 998
QY 447 AATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMLESDDLKTLPTTV 506
DB 999 AATAGQTYRSCMDSTVKYMFYKIPRSVQNRKVTWYETWHSQGMLESSELMVQIPDKM 1058
QY 507 QLALADVNFISIISKVDLFGKCDTQMIYDMLLRLLKSLVLYLPDGFVCKKGEGKEMYLKH 566

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Db 1059 RLDAIDVNYISVSKVALFQGCORQIMFDMLKRLRSVYVLPNDYVCKGSEIGREMYIIQA 1118
 QY 567 GEVQVLGGPDGTQVLTLAGSVFGFISLLAAGGNNRRNTANVAHFANLLTLDKKTLOE 626
 Db 1119 GQVQVLGGPDGKSVLTLAGSVFGFISLLAAGGNNRRNTANVAHFANLLTLDKKTLOE 1178
 QY 627 ILVHPDPSRILMKKARVLLKQKATAEATPPKDLALLFPKKEPPLKFTLLGGTGKA 686
 Db 1179 ILVHPESOKLRLKARRLNKNNK-----PKESVLILPPRAGFPKLFLNAAALAAAGKM 1232
 QY 687 SL-----ARLLKLRQAAKKNSEGGEGEKNEKQKENEKQKENEKQK 734
 Db 1233 GAKGGRGRLALLRLKELAAEAARQQOL---LEQAKSDEDAVGE-----G 1280
 QY 735 KENEDKKGREPEKFLDPECTA-----SPIAVEEPHSVVRTVLP 776
 Db 1281 SASPEQPPRPPAP 1340
 QY 777 RGTSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
 Db 1341 ---EEHPVRIHTLGPDPSEQILLVPEKQEE 1370

RESULT 14

Q4SK9_TETNG
 ID Q4SK9_TETNG PRELIMINARY; PRT; 573 AA.
 AC Q4SK9;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAFI4565, whole genome shotgun sequence.
 DE (fragment).
 GN ORFNames=GSTENG00016673001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
 RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
 RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
 RA Wincker P., Lander E.S., Weissenbach J., Roest Crollius H.
 RT "genome duplication in the teleost fish Tetraodon nigroviridis reveals
 the early vertebrate proto-karyotype."
 RL Nature 431:946-957(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RG Genoscope; Whitehead Institute Centre for Genome Research;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAAE01014565; CAF98823.1; -; Genomic_DNA.
 DR InterPro; IPR00595; cNMP_bd.
 DR InterPro; IPR005821; Ion_trans.
 DR Pfam; PF00027; cNMP_binding; 1.
 DR SMART; SM00100; cNMP; 1.
 DR PROSITE; PS00888; cNMP_BINDING_1; UNKNOWN_1.
 DR PROSITE; PS00888; cNMP_BINDING_2; UNKNOWN_1.
 DR PROSITE; PS00888; cNMP_BINDING_3; 1.
 KW Ion transport; Ionic channel; Transmembrane; Transport.

FT NON_TER 1 573
 FT NON_TER 573
 SQ SEQUENCE 573 AA; 64995 MW; 942B58E39B630BE9 CRC64;
 Query Match 38.7%; Score 1639.5; DB 2; Length 573;
 Best Local Similarity 56.4%; Pred. No. 2.3e-87;
 Matches 326; Conservative 84; Mismatches 149; Indels 19; Gaps 7;
 QY 118 PPAAPVINEYADAQHLNHLVKRQRTALYKKKLVGDDLSPEASPTAKPTAVPPVKESD 177
 Db 1 P P P P P V I N R Y S D E Q L R T I K M R R E L Q I C K D V A D Q Y A S S P P V K S O E A K E R K S V K 60
 QY 178 DXPTHHYRLWFKVKOM--PLTEYLKRIKLPNSIDSYTDRLYLWLLLVLTAYNNCWF 235
 Db 61 ARLTEAY----WSAVDALLEPLEKANDSV-VGVTIDPFTDRRYIAWLSVLTAFNVTWF 115
 QY 236 IFLRLVFPYQTADNIHYMLIADIICDIYLYDMLFIQPRLOFVRGGDIIVDSNELKHYR 295
 Db 116 I T A R L C F P H S P G A V P L M S L D L L A D L V L T D S L V F Q P R K Q F V K A G D I I K D R V M S K K N Y R 175
 QY 296 TSTKFO-LDVASIIIPDICYLFPGNPMFRANRMLKYTSFFFNHLESIMDKAYIRVI 354
 Db 176 ESERFKVLDWALLPFDLLYLQFGPKSIIFRANRLKADAFEFSDRLESIMAKAYIRVI 235
 QY 355 RTGYLLFLHINACVYVWASNYEGITTRWVYDGEENEYLCYYWAVRTLTITIGLPEP 414
 Db 236 RTIGYLLFLHINACVYVWASNYEGITTRWVYDGEENEYLCYYWAVRTLTITIGLPEP 295
 QY 415 QTLFEIVFOLLNFFSGVFVFSLLIGOMRDVIGAATANQNYFRACMDDTIAYMNNYSI 474
 Db 296 HTVFEISFQMTNFTGTVFVFSLLIGOMRDVIGAATAGAYFRSNMONTVAYMVTNRIPS 355
 QY 475 VQKRVTRYEYTWDSQRM-----DESLLKLTPTTVQALAIADVNFPSIISKVDLPK 526
 Db 356 VQNRVTRYTYTWDAQGLQSHAWYQDSSELLDKMPLVMRTAIAVDINLATPKIDLPK 415
 QY 527 GCDTQMIYDMLRLKSVLPGDFVCKGCEIGKEMVIIKHGEVOVLGGDGTQVLTVTLKA 586
 Db 416 GDQQQLVDMLRLKSVLPGDFVCKGCEIGKEMVIIKHGEVOVLGGDGTQVLTVTLKA 475
 QY 587 GSVFGEISLLAAG--GNNRTANVVAHFANLLTLDKKTLOEILVHYPOSERILMKKARV 644
 Db 476 GCVFGEISLLQSKDGGNRTANVKAHFANLVLEKDLFDILVHYPEQVKLARKGRK 535
 QY 645 LKQKA-KTAEATPPRKDLALLFPKKEPPLKFTLLG 681
 Db 536 LMKAGPAAAKVEERKKGLALFGPKPPTPKLLRAFGG 573
 RESULT 15
 Q4T4Q5_TETNG
 ID Q4T4Q5_TETNG PRELIMINARY; PRT; 743 AA.
 AC Q4T4Q5;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
 DE Chromosome undetermined SCAF9565, whole genome shotgun sequence.
 DE (fragment).
 GN ORFNames=GSTENG00007198001;
 OS Tetraodon nigroviridis (Green puffer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
 OC Tetraodontidae; Tetraodontidae; Tetraodon.
 OX NCBI_TaxID=99883;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
 RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
 RA Anhouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
 RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,

RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolious H.,
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAE01009565; CAF92127.1; -; Genomic_DNA.
DR InterPro; IPR005821; Ion trans.
DR Pfam; PF00520; Ion trans; 1
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 743 743
SQ SEQUENCE 743 AA; 83811 MW; 27350BFD6A8D226D CRC64;

Query Match 31.3%; Score 1327; DB 2; Length 743;
Best Local Similarity 40.4%; Pred. No. 5.7e-69;
Matches 277; Conservative 100; Mismatches 186; Indels 122; Gaps 11;

QY 120 AAPVINEYADAAQLHLNLRKMRQRTALYKKLVGGLSSPE----- 159
DB 5 AASVGSVLVQDLRLNQLVSLFKGTERQKERLVDPDESEDAFSACMGPDVDSVTRLQRSKV 64

QY 160 -----ASPOTAKPTAVPPVKESDDKPTHE-----YYRLLMFKVK 193
DB 65 NQLGEALIVGFLISAAPSAAAPPPPPPPPPGDKDEAPAAQAQEDPELPFKILGRPVK 124

QY 194 ----KMPLELYLXRI---KLPSIDSYTDRLYLWLLVTLAYNWCWFIPRLVFPYQTA 247
DB 125 LPRPPLPAWIRLVMEFRFPTSDPYDYYVWLFVVAANWNVWLLIPVMAFPYQTP 184

QY 248 DNIHWYLIADIICDIYLYDMLFIQRLQFVRGGDIIV----- 285
DB 185 DNIHLWLLADYCDLIYIADILLFQTRLQFVRGGDIVGQTDQLRLAFSSASNRVLSQ 244

QY 286 -DSNELRKHRTSTKQDLDAVSIIPDICYLFFGNPMFRANMLKYTSFFFNHLES 344
DB 245 CDRKEMRENYMTDRPKTDLSSLFLELCYIFTGVNPLRFPRLKLYQVFPEFNDMEAV 304

QY 345 MDKAYIYRVIRTTGYLLFTLHINACVYVWASNYEGITTRVYVYDGEENEYLRYYAVRT 404
DB 305 MKKAYIYRVIRTSYLLSLHINACLFYWGSAYEGLGATKWYDGGKNAYIRCYFVAVKT 364

QY 405 LITIGLPEPQTLFEIVFOLLNFFSGVFVSSLIQMDRVIGAAATANQNYFRACMDDTIA 464
DB 365 LITIGLDPPTTVFELCFOLINFYGVFAFSIMIGQMRDVGAATAGENYRACMDSTVK 424

QY 465 YNNYSIPKLQKRVRTWYETWDSQRLMDESLLKTLFTTVQLALADWNFSIISKVDL 524
DB 425 YNNSYIPIQEVQNRKIKTWYDTWKSQMLDEQLLVQLPTKHLDIADVNTIVSRVAL 484

QY 525 PKGCDTQMIYDMLRLKSVLYLPDGFVCKKGKIGKEMWIIKHGEVQVLGGPDGTVLVTIL 584
DB 485 FQCCDRQWVDFMLTRLKSVYVLPDGFVCKKVKTHTHSHSHTLLQ-----RSCNIFVCV 539

QY 585 KAGSVFGEISLLAA---GGGNRRRTANVVAHGFANLITLQKTLQELVHYHVPDSERILMKK 641
DB 540 SGRDRQGDVHQAGRGPGGWSRP-----PDLRHQSW 573

QY 642 ARVLLKQKAKTAEATP---PRKDLALLFP--PKEETPKLFTLLGGTGKASLARLLKLKR 696
DB 574 LVRVGDQLACGRRQPTHQREGSRLRQVHPQGEF-----GGDPGLPRVPEAPP 625

QY 697 EQAAQKENSEGEEGKEDKQK 721

Db 626 QEGQDDADEGQEARTEGRRQRDERR 650
Search completed: December 21, 2005, 19:58:05
Job time : 238 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 19:46:13 ; Search time 186 Seconds
(without alignments)
1911.061 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSTKVNKVPKIGNNEN.....PSAEGGEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4234	100.0	809	5	Aae15982 Human cyc
2	4231	99.9	809	5	Aae15983 Human CNG
3	4231	99.9	809	5	Aae15985 Human CNG
4	4229	99.9	809	5	Aae15984 Human CNG
5	4228	99.9	809	5	Aae15986 Human CNG
6	3217	76.0	615	9	Adz88289 Human CNG
7	1952	46.1	1245	9	Adz88287 Human CNG
8	1949	46.0	909	9	AEAI17267 Human cyc
9	1948.5	46.0	1250	8	ABM83979 Human dia
10	1781.5	42.1	652	4	ABG27471 Novel hum
11	1103	26.1	1037	4	ABG6545 Drosophil
12	1088	25.7	644	4	ABG05466 Novel hum
13	1052.5	24.9	821	9	Adz88294 Human CNG
14	955	22.6	747	4	ABG11969 Novel hum
15	906	21.4	237	6	ABR39396 Amino aci
16	902	21.3	237	6	ABP98584 Amino aci
17	850	20.1	694	5	Aae15987 Human CNG
18	850	20.1	694	7	AAE38591 Human CNG
19	850	20.1	694	9	ADZ88286 Human CNG
20	831.5	19.6	683	7	ADDA48638 Rat Prote
21	829	19.6	663	5	AAG79527 Cow HBMYC
22	829	19.6	663	6	ABG74912 Bovine CN
23	829	19.6	663	9	ADZ88292 Bull CNG
24	826.5	19.5	698	8	ADQ67650 Novel hum

25	825.5	19.5	664	5	AAG79525 Variant H
26	824	19.5	663	6	ABG74914 Bovine CN
27	823	19.4	663	6	ABG74913 Bovine CN
28	821.5	19.4	664	6	ABG72530 Novel hum
29	820.5	19.4	664	5	AAG79524 HBMYCNG.
30	820	19.4	732	5	AAG79526 Rabbit HB
31	820	19.4	732	9	Adz88291 Rabbit CN
32	819.5	19.4	664	4	AAE04894 Human tre
33	819.5	19.4	664	5	ABT78066 Amino aci
34	819.5	19.4	664	6	ABG72529 Novel hum
35	819.5	19.4	664	6	ABU12049 Human NOV
36	819.5	19.4	664	6	ABP98475 Amino aci
37	819.5	19.4	664	9	ADZ88285 Human CNG
38	818.5	19.3	690	7	ADD93244 Cyclic nu
39	818.5	19.3	690	8	ADI38341 Human pro
40	818.5	19.3	690	9	ADZ88284 Human CNG
41	817	19.3	686	7	ADD48640 Human pro
42	816.5	19.3	664	8	ADR09903 Human pro
43	815	19.2	690	5	AAE15988 Human CNG
44	805.5	19.0	664	9	ADZ88293 CNG Chann
45	804	19.0	664	5	AAG79529 Rat HBMYC

ALIGNMENTS

RESULT 1
AAE15982
ID AAE15982 standard; protein; 809 AA.
XX
AC AAE15982;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human cyclic nucleotide-gated cation channel 3 beta subunit protein.
XX
KW Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
KW Cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
KW male infertility; genetic defect; reporter-ligand interaction; CNG;
KW viral infection; cancer.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 210..661
FT /note= "Conserved region; this region also function as an
FT epitope and is referred in claim 1"
XX
PN WO200188090-A2.
XX
PD 22-NOV-2001.
XX
PF 15-MAY-2001; 2001WO-US015814.
XX
PR 15-MAY-2000; 2000US-0204445P.
PR 14-MAY-2001; 2001US-00853828.
XX
(ICAG-) ICAGEN INC.
XX
PI Creech CD, Jegla TJ;
XX
DR WPI; 2002-089847/12.
DR N-PSDB; AAD25729.
XX
XX New polypeptide, useful for screening for modulators of cyclic nucleotide-gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit.
PT
PT Claim 12; Fig 4; 83pp; English.
XX
PS The invention relates to human cyclic nucleotide-gated cation channel 3
XX beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
CC of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms

CC	functional heteromultimers with CNGA1 and/or CNGA3, two CNG alpha
CC	subunits that are expressed in retina. CNG3B polypeptides are useful for
CC	screening modulators of CNGs which are useful as contraceptives and for
CC	treating various disorders involving cation channels, e.g. vision
CC	disorders and male infertility. Polynucleotides of the invention are
CC	useful for transfection of cells in vitro and in vivo, to correct
CC	acquired and inherited genetic defects, cancer and viral infections.
CC	Sequences of the invention are useful as reporter molecules in assays and
CC	detection systems, to measure changes in cation concentration, membrane
CC	potential, current flow, ion flux, transcription, signal transduction, in
CC	reporter-ligand interactions and second messenger concentrations, in
CC	vitro, in vivo and ex vivo. They are useful to construct models of CNGs
CC	in a computer system and for examining expression and regulation of
CC	cation channels. The present sequence is human CNG3B protein
xx	
SQ	Sequence 809 AA;
	Query Match 100.0%; Score 4234; DB 5; Length 809;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 809; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 MFKSLTKVKVKPIGENNENQSSRRNEEGSHPSNQSOQTTAQENKGEESLTKTKSPV 60
Db	1 MFKSLTKVKVKPIGENNENQSSRRNEEGSHPSNQSOQTTAQENKGEESLTKTKSPV 60
Qy	61 TSEBPHNIIQDKLSKQSSGDLTTNPDQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPA 120
Db	61 TSEBPHNIIQDKLSKQSSGDLTTNPDQNAAEPTGTVPEQKEMDPGKEGPNSPQNKPPA 120
Qy	121 APVINEVADAQLHNLVKRMORTALYKKKLVEGDLSSEASPSQTAKPATVPVKESDDPK 180
Db	121 APVINEVADAQLHNLVKRMORTALYKKKLVEGDLSSEASPSQTAKPATVPVKESDDPK 180
Qy	181 TEHYRLLWFVKVKMPLTEYLKRIKLPSIDSYTDRLYLLMLLVTLAYNNWCNFIPLRL 240
Db	181 TEHYRLLWFVKVKMPLTEYLKRIKLPSIDSYTDRLYLLMLLVTLAYNNWCNFIPLRL 240
Qy	241 VFPYQTADNIHWLIADIICDIIYLYDMLFTQPRLQFVRGGDIIVDSNELRGHVRTSTPKF 300
Db	241 VFPYQTADNIHWLIADIICDIIYLYDMLFTQPRLQFVRGGDIIVDSNELRGHVRTSTPKF 300
Qy	301 QLDVASIIPDICIYLFYGFNPFMRNMLKVTSTFEFNHLESIMDKAYIVRVIRTTGYL 360
Db	301 QLDVASIIPDICIYLFYGFNPFMRNMLKVTSTFEFNHLESIMDKAYIVRVIRTTGYL 360
Qy	361 LFIILHINACVYWASNYEGITTRWYVDGEGNEYLRCYWAVRTLIITIGGLPEPQTLFEI 420
Db	361 LFIILHINACVYWASNYEGITTRWYVDGEGNEYLRCYWAVRTLIITIGGLPEPQTLFEI 420
Qy	421 VFQLLNFFSGVFPVSSILIGQRDVI GAATANQNTFPRACMDDTIAYMNNYSIPKLQVKRVR 480
Db	421 VFQLLNFFSGVFPVSSILIGQRDVI GAATANQNTFPRACMDDTIAYMNNYSIPKLQVKRVR 480
Qy	481 TWSEYTWDSQRMLDESLLKTLPTTVQLALAI DVNFSII SKVDLFFKGC DTQMI VDM LRL 540
Db	481 TWSEYTWDSQRMLDESLLKTLPTTVQLALAI DVNFSII SKVDLFFKGC DTQMI VDM LRL 540
Qy	541 KSVLYLPDGFVCKKGEIGKEMYYIIKHGEVQVVGPDGTVKLVITLKAGSVFGEISLLAAGG 600
Db	541 KSVLYLPDGFVCKKGEIGKEMYYIIKHGEVQVVGPDGTVKLVITLKAGSVFGEISLLAAGG 600
Qy	601 GNRRTANVAHGFANLITLDKKTLOEILVHVPDSEIRILMKARVLLKQAKTAETATPRK 660
Db	601 GNRRTANVAHGFANLITLDKKTLOEILVHVPDSEIRILMKARVLLKQAKTAETATPRK 660
Qy	661 DLALLFPFKBETPKLFTLLGGTGKASLARLLKLRQAAOKKENSEGEEGKENEKDQ 720
Db	661 DLALLFPFKBETPKLFTLLGGTGKASLARLLKLRQAAOKKENSEGEEGKENEKDQ 720
Qy	721 KENEDKQKENEKQKENEKDKGREPEKPLDRPECTASPIAVBEEPHSVRVTLPRTGS 780
Db	721 KENEDKQKENEKQKENEKDKGREPEKPLDRPECTASPIAVBEEPHSVRVTLPRTGS 780

		Matches	808;	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MPKSLTKVNVKVP	IGENNENEGSSRRNEGSHPSNQSQTTAQEENKGBEKS	LTKSTPV	60						
Db	1	MPKSLTKVNVKVP	IGENNENEGSSRRNEGSHPSNQSQTTAQEENKGBEKS	LTKSTPV	60						
Qy	61	TSEEPHTNIQDKLS	KNSSGDLTTNPD	PQNAASPTGTVPEQEMDPGKGGPNSPQNKPPA	120						
Db	61	TSEEPHTNIQDKLS	KNSSGDLTTNPD	PQNAASPTGTVPEQEMDPGKGGPNSPQNKPPA	120						
Qy	121	APVINEYADAQLHNLVKRMQR	TALYKKKLVEGDLSSPEAS	POTAKPTAVPPVKESDDKP	180						
Db	121	APVINEYADAQLHNLVKRMQR	TALYKKKLVEGDLSSPEAS	POTAKPTAVPPVKESDDKP	180						
Qy	181	TEHYRLLWPKVKKMP	LTLEYLKRILKIPNSIDSVTDRLYLWLLVLTAYNNWNCWF	PLRL	240						
Db	181	TEHYRLLWPKVKKMP	LTLEYLKRILKIPNSIDSVTDRLYLWLLVLTAYNNWNCWF	PLRL	240						
Qy	241	VFPYQTADNTHYWL	ADIICDIILYDMLFIQRLQFVRGGDIIVDSNELRKHYRTSTKF	300							
Db	241	VFPYQTADNTHYWL	ADIICDIILYDMLFIQRLQFVRGGDIIVDSNELRKHYRTSTKF	300							
Qy	301	QLDVASIIIPDICYL	FGFNPFRANMLKYTSFFFNHLSIMDKAYIYRVRTTGYL	360							
Db	301	QLDVASIIIPDICYL	FGFNPFRANMLKYTSFFFNHLSIMDKAYIYRVRTTGYL	360							
Qy	361	LFILHINACYYWAS	YVGGITRWYVYDGEENYLCYYWAVRTLITIGGLPEPQTLFEI	420							
Db	361	LFILHINACYYWAS	YVGGITRWYVYDGEENYLCYYWAVRTLITIGGLPEPQTLFEI	420							
Qy	421	VPOLLNPFSGV	FVSSLIQMRDVI GAATANQNYFRACMDDTIAYNNYSIPKL	VOKRVR	480						
Db	421	VPOLLNPFSGV	FVSSLIQMRDVI GAATANQNYFRACMDDTIAYNNYSIPKL	VOKRVR	480						
Qy	481	TWTEYTWDSOR	MLDESLLKTLPTVQLALAI	DVNFSSIIKVDLFGKCDTQMIYDMLLRL	540						
Db	481	TWTEYTWDSOR	MLDESLLKTLPTVQLALAI	DVNFSSIIKVDLFGKCDTQMIYDMLLRL	540						
Qy	541	KSVLYLPGD	PVCKKGEIGKEMYIKHGEVQVLGGPDGTVLTKAGSVFGEIS	LAAAGG	600						
Db	541	KSVLYLPGD	PVCKKGEIGKEMYIKHGEVQVLGGPDGTVLTKAGSVFGEIS	LAAAGG	600						
Qy	601	GNRRTANVAHG	FANLLTLDKTLQELVHYPSERILMKARVLLKOKAKTA	EATPPRK	660						
Db	601	GNRRTANVAHG	FANLLTLDKTLQELVHYPSERILMKARVLLKOKAKTA	EATPPRK	660						
Qy	661	DLALLFPK	ETPKLFTLLGGTGKASLARLLKREOAAQKKNSSGEGEENEDKQ	720							
Db	661	DLALLFPK	ETPKLFTLLGGTGKASLARLLKREOAAQKKNSSGEGEENEDKQ	720							
Qy	721	KENEDKQ	KENEDKDKGREPEEKPLDRPECTASPIAVEEHPHVRRTVLP	PGTS	780						
Db	721	KENEDKQ	KENEDKDKGREPEEKPLDRPECTASPIAVEEHPHVRRTVLP	PGTS	780						
Qy	781	RQSLIISMAPS	AEGBEVLTEVKEKAKQ	809							
Db	781	RQSLIISMAPS	AEGBEVLTEVKEKAKQ	809							

RESULT 3

ID	AAE15985	standard; protein; 809 AA.
XX	AAE15985;	
AC	AAE15985;	
DT	26-MAR-2002	(first entry)
XX	Human CNG3B	protein variant #3 (L675V).
XX	Human;	cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
KW	cyclic nucleotide-gated ion channel;	contraceptive; vision disorder;
KW	male infertility; genetic defect;	reporter-ligand interaction; CNG;
KW	viral infection; cancer; mutant;	mutant; variant.

XX	Homo sapiens.	
OS	Synthetic.	
XX	Key	Location/Qualifiers
FT	Misc-difference 675	/note= "Wild type Leu substituted with Val"
XX	WO200188090-A2.	
XX	22-NOV-2001.	
XX	15-MAY-2001;	2001WO-US015814.
XX	15-MAY-2000;	2000US-0204445P.
PR	14-MAY-2001;	2001US-0085582B.
XX	(ICAG-) ICAGEN INC.	
XX	Crech CD, Jegla TJ;	
XX	WPI; 2002-089847/12.	
XX	New polypeptide, useful for screening for modulators of cyclic nucleotide	
PT	gated ion channels, comprises the isolated cyclic nucleotide-gated	
PT	cation channel 3 beta subunit.	
XX	Disclosure; Page; 83pp; English.	
XX	The invention relates to human cyclic nucleotide-gated cation channel 3	
CC	beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member	
CC	of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms	
CC	functional heteromultimers with CNGA1 and/or CNGB3. Two CNG alpha	
CC	subunits that are expressed in retina. CNG3B polypeptides are useful for	
CC	screening modulators of CNGs which are useful as contraceptives and for	
CC	treating various disorders involving cation channels, e.g. vision	
CC	disorders and male infertility. Polynucleotides of the invention are	
CC	useful for transfection of cells in vitro and in vivo, to correct	
CC	acquired and inherited genetic defects, cancer and viral infections.	
CC	Sequences of the invention are useful as reporter molecules in assays and	
CC	detection systems, to measure changes in cation concentration, membrane	
CC	potential, current flow, ion flux, transcription, signal transduction,	
CC	reporter-ligand interactions and second messenger concentrations. In	
CC	vitro, in vivo and ex vivo. They are useful to construct models of CNGs	
CC	in a computer system and for examining expression and regulation of	
CC	cation channels. The present sequence is human CNG3B protein variant	
CC	(L675V). Note: This sequence is not shown in the specification, but is	
CC	derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig	
CC	4 of the specification (AAE15982)	
XX	Sequence 809 AA;	

Query Match	99.9%;	Score 4231;	DB 5;	Length 809;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches	808;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;

Qy	1	MPKSLTKVNVKVP	IGENNENEGSSRRNEGSHPSNQSQTTAQEENKGBEKS	LTKSTPV	60
Db	1	MPKSLTKVNVKVP	IGENNENEGSSRRNEGSHPSNQSQTTAQEENKGBEKS	LTKSTPV	60
Qy	61	TSEEPHTNIQDKLS	KNSSGDLTTNPD	PQNAASPTGTVPEQEMDPGKGGPNSPQNKPPA	120
Db	61	TSEEPHTNIQDKLS	KNSSGDLTTNPD	PQNAASPTGTVPEQEMDPGKGGPNSPQNKPPA	120
Qy	121	APVINEYADAQLHNLVKRMQR	TALYKKKLVEGDLSSPEAS	POTAKPTAVPPVKESDDKP	180
Db	121	APVINEYADAQLHNLVKRMQR	TALYKKKLVEGDLSSPEAS	POTAKPTAVPPVKESDDKP	180
Qy	181	TEHYRLLWPKVKKMP	LTLEYLKRILKIPNSIDSVTDRLYLWLLVLTAYNNWNCWF	PLRL	240
Db	181	TEHYRLLWPKVKKMP	LTLEYLKRILKIPNSIDSVTDRLYLWLLVLTAYNNWNCWF	PLRL	240
Qy	241	VFPYQTADNTHYWL	ADIICDIILYDMLFIQRLQFVRGGDIIVDSNELRKHYRTSTKF	300	

Db	241	VFPYQTADNIHWLIADIICDIYLYDMLFIQPRQLQFVRGGDIIVDSNELRKHRTSTKF	300
Qy	301	QLDVASIIPFDICYLFFGFGNPFMRANMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL	360
Db	301	QLDVASIIPFDICYLFFGFGNPFMRANMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL	360
Qy	361	LFILHINACVYVWASNYEGIGTRWYVYDGEYLRCCYYWAVRTLITIGGLPEPOTLFEI	420
Db	361	LFILHINACVYVWASNYEGIGTRWYVYDGEYLRCCYYWAVRTLITIGGLPEPOTLFEI	420
Qy	421	VFQLNFFSGVVFSSLIQMRDVGAATANQNYFRACDDTIAYNNYSIPKLQVKRVR	480
Db	421	VFQLNFFSGVVFSSLIQMRDVGAATANQNYFRACDDTIAYNNYSIPKLQVKRVR	480
Qy	481	TWYEYTWDSQRMDESLLKTLPTTVQALAIQVNFNFSIIKVDLPKGCDDTQIYDMLLRL	540
Db	481	TWYEYTWDSQRMDESLLKTLPTTVQALAIQVNFNFSIIKVDLPKGCDDTQIYDMLLRL	540
Qy	541	KSVLYLPGDFVCKGKEIGKEMVIIKHGEVQVLGGPDGTVLTLKAGSVFGEISLLAAGS	600
Db	541	KSVLYLPGDFVCKGKEIGKEMVIIKHGEVQVLGGPDGTVLTLKAGSVFGEISLLAAGS	600
Qy	601	GNRRANVVAHFANLLTLDKTQLQBIIVHYDPDSERILMKKARVLLKQAKTAETPPRK	660
Db	601	GNRRANVVAHFANLLTLDKTQLQBIIVHYDPDSERILMKKARVLLKQAKTAETPPRK	660
Qy	661	DLALLFPKKEETPKFKTLGGTGKASLARLLKREQAOKKENSEGGESEKGENEDKQ	720
Db	661	DLALLFPKKEETPKFKTLGGTGKASLARLLKREQAOKKENSEGGESEKGENEDKQ	720
Qy	721	KENEDQKENEKGENEDKQGREPEEKPLDRPECTASPIAVEBEPHSVRVTLPRGTS	780
Db	721	KENEDQKENEKGENEDKQGREPEEKPLDRPECTASPIAVEBEPHSVRVTLPRGTS	780
Qy	781	RQSLIISMAPSREGGEVLTIIEVKEKAKQ	809
Db	781	RQSLIISMAPSREGGEVLTIIEVKEKAKQ	809
RESULT 4			
AAE15984			
ID	AAE15984 standard; protein; 809 AA.		
XX			
AC	AAE15984;		
DT			
DT			
XX	26-MAR-2002 (first entry)		
XX			
DE	Human CNG3B protein variant #2 (D154N).		
XX			
KW	Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;		
KW	cyclic nucleotide-gated ion channel; contraceptive; vision disorder;		
KW	male infertility; genetic defect; reporter-ligand interaction; CNG;		
XX	viral infection; cancer; mutant; mutein; variant.		
OS	Homo sapiens.		
OS	Synthetic.		
FH	Key Location/Qualifiers		
FT	Misc-difference 154		
FT	/note= "wild type Asp substituted with Asn"		
XX			
PN	WO200108090-A2.		
XX			
PD	22-NOV-2001.		
XX			
PF	15-MAY-2001; 2001WO-US015814.		
XX			
PR	15-MAY-2000; 2000US-0204445P.		
PR	14-MAY-2001; 2001US-00855828.		
XX			
PA	(ICAG-) ICAGEN INC.		
XX			

PI	Crech CD, Jegla TJ;			
XX				
DR	WPI; 2002-089847/12.			
XX				
PT	New polypeptide, useful for screening for modulators of cyclic nucleotide-gated ion channels, comprises the isolated cyclic nucleotide-gated cation channel 3 beta subunit.			
PT				
XX				
PS	Disclosure; Page; 83pp; English.			
XX				
CC	The invention relates to human cyclic nucleotide-gated cation channel 3 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha subunits that are expressed in retina. CNG3B polypeptides are useful for screening modulators of CNGs which are useful as contraceptives and for treating various disorders involving cation channels, e.g. vision disorders and male infertility. Polynucleotides of the invention are useful for transfection of cells in vitro and in vivo, to correct acquired and inherited genetic defects, cancer and viral infections. Sequences of the invention are useful as reporter molecules in assays and detection systems, to measure changes in cation concentration, membrane potential, current flow, ion flux, transcription, signal transduction, reporter-ligand interactions and second messenger concentrations, in vitro, in vivo and ex vivo. They are useful to construct models of CNGs in a computer system and for examining expression and regulation of cation channels. The present sequence is human CNG3B protein variant (D154N). Note: This sequence is not shown in the specification, but is derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig 4 of the specification (AAE15982)			
XX				
SQ	Sequence 809 AA;			
	Query Match	99.9%;	Score 4229;	DB 5; Length 809;
	Best Local Similarity	99.9%;	Pred. No. 0;	
PS	Matches 808;	Conservative 1;	Mismatches 0;	Indels 0; Gaps 0;
QY	1	MFKSLTKVNVKPIGNNENEGSSRRNEEGSHPSNQSOOTTAQENKGEESLTKSTPV	60	
DB	1	MFKSLTKVNVKPIGNNENEGSSRRNEEGSHPSNQSOOTTAQENKGEESLTKSTPV	60	
QY	61	TSEEPHTNIQDKLSKKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKGNPNKPKPA	174	
DB	61	TSEEPHTNIQDKLSKKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKGNPNKPKPA	174	
QY	121	APVINEYADAQHNLVKRMORTALYKKLVGEGDSSPEASPTAKPTAVPVKESDDKP	180	
DB	121	APVINEYADAQHNLVKRMORTALYKKLVGEGDSSPEASPTAKPTAVPVKESDDKP	180	
QY	181	TEHYRLLWFVKVMPLTEYLKRIKLPSIDSYDRLVLLMLLVTLAYNNCWFIPLRL	240	
DB	181	TEHYRLLWFVKVMPLTEYLKRIKLPSIDSYDRLVLLMLLVTLAYNNCWFIPLRL	240	
QY	241	VFPYQTADNIHWLIADIICDIYLYDMLFIQPRQLQFVRGGDIIVDSNELRKHRTSTKF	300	
DB	241	VFPYQTADNIHWLIADIICDIYLYDMLFIQPRQLQFVRGGDIIVDSNELRKHRTSTKF	300	
QY	301	QLDVASIIPFDICYLFFGFGNPFMRANMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL	360	
DB	301	QLDVASIIPFDICYLFFGFGNPFMRANMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYL	360	
QY	361	LFILHINACVYVWASNYEGIGTRWYVYDGEYLRCCYYWAVRTLITIGGLPEPOTLFEI	420	
DB	361	LFILHINACVYVWASNYEGIGTRWYVYDGEYLRCCYYWAVRTLITIGGLPEPOTLFEI	420	
QY	421	VFQLNFFSGVVFSSLIQMRDVGAATANQNYFRACDDTIAYNNYSIPKLQVKRVR	480	
DB	421	VFQLNFFSGVVFSSLIQMRDVGAATANQNYFRACDDTIAYNNYSIPKLQVKRVR	480	
QY	481	TWYEYTWDSQRMDESLLKTLPTTVQALAIQVNFNFSIIKVDLPKGCDDTQIYDMLLRL	540	
DB	481	TWYEYTWDSQRMDESLLKTLPTTVQALAIQVNFNFSIIKVDLPKGCDDTQIYDMLLRL	540	

Qy 541 KSVLYLPDGFVCKKGIGKEMYYIKHGEVQVLGGPDGTVKLVTLKAGSVFGEISLLAAGG 600
 Db 541 KSVLYLPDGFVCKKGIGKEMYYIKHGEVQVLGGPDGTVKLVTLKAGSVFGEISLLAAGG 600
 Qy 601 GNRRTANVAHGFANLLTLDKKTQBLVHYVPSERILMKKARVLLKQAKATAEATPPRK 660
 Db 601 GNRRTANVAHGFANLLTLDKKTQBLVHYVPSERILMKKARVLLKQAKATAEATPPRK 660
 Qy 661 DLALLPPKBEETPKLFTKLLGGTGKASLARLLKREQAQKKEGEGEENEDKQ 720
 Db 661 DLALLPPKBEETPKLFTKLLGGTGKASLARLLKREQAQKKEGEGEENEDKQ 720
 Qy 721 KENEDKQKENEKEDKQKREPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780
 Db 721 KENEDKQKENEKEDKQKREPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780
 Qy 781 RQSLIISMAPSAGGEBEVLTIIEVKEKAKQ 809
 Db 781 RQSLIISMAPSAGGEBEVLTIIEVKEKAKQ 809

RESULT 5

AAE15986
 ID AAE15986 standard; protein; 809 AA.

AC AAE15986;

DT 26-MAR-2002 (first entry)

DE Human CNG3B protein variant #4 (G682S).

Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;
 cyclic nucleotide-gated ion channel; contraceptive; vision disorder;
 male infertility; Genetic defect; reporter-ligand interaction; CNG;
 viral infection; cancer; mutant; mutein; variant.

OS Homo sapiens.
 Synthetic.

Key Location/Qualifiers

Key Misc-difference 682 /note= "Wild type Gly substituted with Ser"

WO200188090-A2.

22-NOV-2001.

15-MAY-2001; 2001WO-US015814.

15-MAY-2000; 2000US-0204445P.

14-MAY-2001; 2001US-00855828.

(ICAG-) ICAGEN INC.

Crech CD, Jegla TJ;

WPI; 2002-089847/12.

New polypeptide, useful for screening for modulators of cyclic nucleotide
 -gated ion channels, comprises the isolated cyclic nucleotide-gated
 cation channel 3 beta subunit.

Disclosure; Page; 83pp; English.

The invention relates to human cyclic nucleotide-gated cation channel 3
 beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member
 of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms
 functional heteromultimers with CNGA1 and/or CNGB3, two CNG alpha
 subunits that are expressed in retina. CNG3B polypeptides are useful for
 screening modulators of CNGs which are useful as contraceptives and for
 treating various disorders involving cation channels, e.g. vision
 disorders and male infertility. Polynucleotides of the invention are
 useful for transfection of cells in vitro and in vivo, to correct

CC acquired and inherited genetic defects, cancer and viral infections.
 CC Sequences of the invention are useful as reporter molecules in assays and
 CC detection systems, to measure changes in cation concentration, membrane
 CC potential, current flow, ion flux, transcription, signal transduction,
 CC reporter-ligand interactions and second messenger concentrations, in
 CC vitro, in vivo and ex vivo. They are useful to construct models of CNGs
 CC in a computer system and for examining expression and regulation of
 CC cation channels. The present sequence is human CNG3B protein variant
 CC (G682S). Note: This sequence is not shown in the specification, but is
 CC derived from the human wild type CNG3B protein (SEQ ID NO:1) shown in Fig
 CC 4 of the specification (AAE15982)

XX Sequence 809 AA;

Query Match 99.9%; Score 4228; DB 5; Length 809;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 808; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MFKSLTKVNVKVPKIGENNENESSRRENEEGSHPSNOSQOTTAQENKGEKSLTKSTPV 60
 Db 1 MFKSLTKVNVKVPKIGENNENESSRRENEEGSHPSNOSQOTTAQENKGEKSLTKSTPV 60
 Qy 61 TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTCTVPEQKEMDPGKGNPSPONKPPA 120
 Db 61 TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTCTVPEQKEMDPGKGNPSPONKPPA 120
 Qy 121 APVINEYADAQLHNLVKRMQRORTALYKKLVKVEGDLSSPEASPOKAPTAVPPVKESDDKP 180
 Db 121 APVINEYADAQLHNLVKRMQRORTALYKKLVKVEGDLSSPEASPOKAPTAVPPVKESDDKP 180
 Qy 181 TEHYELLAFKVKKMPLETKLIPNSIDSTYDRLLYLLWLLVTLAYNNWCWFPLRL 240
 Db 181 TEHYELLAFKVKKMPLETKLIPNSIDSTYDRLLYLLWLLVTLAYNNWCWFPLRL 240
 Qy 241 VFPYQADNHIHYWLIADIIICDIIYLYDMLFIQRLQFVRGGDIIVDSNELKHYRTSTKF 300
 Db 241 VFPYQADNHIHYWLIADIIICDIIYLYDMLFIQRLQFVRGGDIIVDSNELKHYRTSTKF 300
 Qy 301 QLDVASIIPFDICYLFFGNPMFRANRMLKYTSFFFNHLESIMDKAYIYRVIRTTGYL 360
 Db 301 QLDVASIIPFDICYLFFGNPMFRANRMLKYTSFFFNHLESIMDKAYIYRVIRTTGYL 360
 Qy 361 LFTLHINACVYWASNYEGITTRWYDGEENYLCYCWAVRTLITIGGLPBPOTLFEI 420
 Db 361 LFTLHINACVYWASNYEGITTRWYDGEENYLCYCWAVRTLITIGGLPBPOTLFEI 420
 Qy 421 VFOLLNFFSGVVFSSLIQOMRDVIGAATANQNYFRACMDDTIAYMNNYSI PKLVOKRVR 480
 Db 421 VFOLLNFFSGVVFSSLIQOMRDVIGAATANQNYFRACMDDTIAYMNNYSI PKLVOKRVR 480
 Qy 481 TWYEYTWDSQRMLESDDLKTLPTTVQALAI DVNFSIISKVDLFKGCDDTOMIYDMLLRL 540
 Db 481 TWYEYTWDSQRMLESDDLKTLPTTVQALAI DVNFSIISKVDLFKGCDDTOMIYDMLLRL 540
 Qy 541 KSVLYLPDGFVCKKGIGKEMYYIKHGEVQVLGGPDGTVKLVTLKAGSVFGEISLLAAGG 600
 Db 541 KSVLYLPDGFVCKKGIGKEMYYIKHGEVQVLGGPDGTVKLVTLKAGSVFGEISLLAAGG 600
 Qy 601 GNRRTANVAHGFANLLTLDKKTLOEILVHYVPSERILMKKARVLLKQAKATAEATPPRK 660
 Db 601 GNRRTANVAHGFANLLTLDKKTLOEILVHYVPSERILMKKARVLLKQAKATAEATPPRK 660
 Qy 661 DLALLPPKBEETPKLFTKLLGGTGKASLARLLKREQAQKKEGEGEENEDKQ 720
 Db 661 DLALLPPKBEETPKLFTKLLGGTGKASLARLLKREQAQKKEGEGEENEDKQ 720
 Qy 721 KENEDKQKENEKEDKQKREPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780
 Db 721 KENEDKQKENEKEDKQKREPEEKPLDRPECTASPIAVEEPHSHVRRVTLPRGTS 780
 Qy 781 RQSLIISMAPSAGGEBEVLTIIEVKEKAKQ 809
 Db 781 RQSLIISMAPSAGGEBEVLTIIEVKEKAKQ 809

RESULT 6
ADZ88289
ID ADZ88289 standard; protein; 615 AA.
XX
AC ADZ88289;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human CNG channel CNGB3.
XX
KW antiasthmatic; Antiallergic; Hypotensive; Gastrointestinal-Gen.;
KW Antiparkinsonian; Antidepressant; Neuroleptic; Cardiant; GPCR-Antagonist;
KW Unspecified GPCR; cyclic nucleotide-gated channel A2; CNCA2; CNG;
KW mutation; divalent cation-mediated blockage; cation flux;
KW G-protein coupled receptor; asthma; hypertension; allergic reaction;
KW Parkinsons disease; depression; schizophrenia; heart disease.
XX
OS Homo sapiens.
XX
PN WO2005041758-A2.
XX
PD 12-MAY-2005.
XX
PF 01-NOV-2004; 2004WO-US036022.
XX
PR 30-OCT-2003; 2003US-0515442P.
XX
PR 20-JUL-2004; 2004US-0589012P.
XX
PA (ATTO-) ATTO BIOSCIENCE INC.
XX
PI Yao Y, Cao L, Lu J, Llorente I;
XX
DR WPI; 2005-366496/37.
XX
XX
PT New isolated polynucleotide encoding a mutant cyclic nucleotide-gated
PT (CNG) channel having a mutation that decreases divalent cation-mediated
PT blockage of cation flux, and makes the channel more sensitive to cAMP.
XX
PS Disclosure; SEQ ID NO 14; 156pp; English.
XX
CC This sequence represents a wild type human cyclic nucleotide-gated (CNG)
CC channel. The rat CNG channel sequence, CNCA2, may be mutated to form the
CC isolated polynucleotide of the invention which comprising a sequence
CC encoding a mutant CNG channel comprising at least one mutation that
CC decreases divalent cation-mediated blockage of cation flux, and at least
CC one mutation that makes the channel more sensitive to cAMP than a channel
CC that does not comprise the mutation. The invention includes methods for:
CC (a) detecting changes in intracellular levels of cAMP, comprising
CC expressing in a cell the polynucleotide cited above, and measuring
CC activity of the channel, where activity of the channel is indicative of
CC changes in intracellular cAMP; (b) detecting activity of a GPCR,
CC comprising expressing the CNG channel and the G-protein coupled receptor
CC (GPCR) in host cell transformed with the nucleotide of the invention, and
CC measuring activity of the channel, where activity of the channel
CC indicates activity of the GPCR; (c) identifying a ligand for a receptor,
CC comprising contacting a cell with a compound wherein the cell expresses
CC the receptor and the mutant CNG channel cited above, and measuring
CC activation of the CNG channel, where activation of the CNG channel
CC indicates that the compound is a ligand for the receptor; (d) identifying
CC an agent that modulates an activity mediated by a GPCR, comprising
CC contacting the transformed host cell with the agent and a ligand for the
CC receptor, and measuring activation of the CNG channel. The methods and
CC compositions of the present invention are useful in cellular physiology,
CC in particular for cell-based assays that employ cation and voltage-based
CC dyes and other indicators, including novel CNG mutants for cyclic
CC nucleotide assays, and for measuring the activity of GPCR in disorders
CC such as asthma, hypertension, allergic reactions, gastrointestinal
CC disorders, Parkinson's disease, depression, schizophrenia and heart
CC disease. This sequence was included in the specification for comparison
CC purposes.

SQ Sequence 615 AA;

Query Match 76.0%; Score 3217; DH 9; Length 615.
Best Local Similarity 100.0%; Pred. No. 2.4e-265;
Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 195 MPLTEYLKRIKLPNSIDSYTDRLYLMLLLVLTAYNNWCWFIPFLRVFPYQTADNIHWL 254
DB 1 MPLTEYLKRIKLPNSIDSYTDRLYLMLLLVLTAYNNWCWFIPFLRVFPYQTADNIHWL 60
QY 255 IADIICDIILYLDMLFIQPLQFVRGGDIIVDSNELRKHYRTSTKFOLDVASIIFPDICY 314
DB 61 IADIICDIILYLDMLFIQPLQFVRGGDIIVDSNELRKHYRTSTKFOLDVASIIFPDICY 120
QY 315 LFFGPNPFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYLLFILHINACVYWA 174
DB 131 LFFGPNPFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYLLFILHINACVYWA 180
QY 375 SNYEGIGTRWYVDGEGNEYLRCYYWAVRTLITIGLPEPOTLFEIVFQLNFFSGVFVF 434
DB 181 SNYEGIGTRWYVDGEGNEYLRCYYWAVRTLITIGLPEPOTLFEIVFQLNFFSGVFVF 240
QY 435 SSLIGQMRDVI GAATANQNYFRACMDDTIAYNNYSIPKLVQKRVRTWYETWDSQRMLD 494
DB 241 SSLIGQMRDVI GAATANQNYFRACMDDTIAYNNYSIPKLVQKRVRTWYETWDSQRMLD 300
QY 495 ESDLLKTLPTTVQLALADIVNFSIISKVDLPFGCDTQMIYDMLLRKSVLYLPGDFVCKK 554
DB 301 ESDLLKTLPTTVQLALADIVNFSIISKVDLPFGCDTQMIYDMLLRKSVLYLPGDFVCKK 360
QY 555 GEIGKEMYIIKHGEVQVLGGPDGTVLTKAGSVFGEISLLAAGGNNRRNTANVVAHGFA 614
DB 361 GEIGKEMYIIKHGEVQVLGGPDGTVLTKAGSVFGEISLLAAGGNNRRNTANVVAHGFA 420
QY 615 NLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRKDLALLFPPEETPK 674
DB 421 NLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRKDLALLFPPEETPK 480
QY 675 LFKTLGGTGKASLARLLKREQAOKKENSEGEGEKGKENEKOKENEKOKENEKOK 734
DB 481 LFKTLGGTGKASLARLLKREQAOKKENSEGEGEKGKENEKOKENEKOKENEKOK 544
QY 735 KENEDKDKGRPEEKPLDRPECTASPIAVEEPHSVRRTVLPRTGTSROSLIISMAPSARG 794
DB 541 KENEDKDKGRPEEKPLDRPECTASPIAVEEPHSVRRTVLPRTGTSROSLIISMAPSARG 600
QY 795 GEEVLTIEVKEKAQ 809
DB 601 GEEVLTIEVKEKAQ 615
RESULT 7
ADZ88287
ID ADZ88287 standard; protein; 1245 AA.
XX
AC ADZ88287;
XX
DT 14-JUL-2005 (first entry)
XX
DE Human CNG channel CNGB1.
XX
KW antiasthmatic; Antiallergic; Hypotensive; Gastrointestinal-Gen.;
KW Antiparkinsonian; Antidepressant; Neuroleptic; Cardiant; GPCR-Antagonist;
KW Unspecified GPCR; cyclic nucleotide-gated channel A2; CNCA2; CNG;
KW mutation; divalent cation-mediated blockage; cation flux;
KW G-protein coupled receptor; asthma; hypertension; allergic reaction;
KW Parkinsons disease; depression; schizophrenia; heart disease.
XX
OS Homo sapiens.
XX
PN WO2005041758-A2.
XX
PD 12-MAY-2005.

Query Match	46.08;	Score 1948.5;	DB 8;	Length 1250;
Best Local Similarity	46.21;	Pred. No. 1.6e-156;		
Matches	403;	Conservative 125;	Mismatches 235;	Indels 109; Gaps 18;
Qy	14	IGENNENEQSRNNEEGSHPSNOSQOQTAGE---ENKGE---EKSLTKTSPTVTSEEPTHN	68	
Db	409	VGEAEKKEAEKAEAEVAAEEAEKPEQDMAETKEEPEAEAEAASSGVPAHKQHEVQ	468	
Qy	69	IQDK-----LSKNGSGDLTNPDPQNAABPTGTVP-----E0KE	103	
Db	469	VEDTDADSCPLMAEENPPS---TVLPPSPAKSDTLIVPSSASGTHKKLPSEDEAEELKA	526	
Qy	104	MDPKG-----EGNSPON-----KPPAAPVINEVADALQHNLVKRMQORTALYK	147	
Db	527	LSPAESPVAWSDETTTKDTGGQDRAASTASTNSAIIND---RLQELVKLFKERTKVK	582	
Qy	148	KKLVEGDLS----SPEASPTAKPTAVPPVKESDDKPT--EHYVRLLMFVKVKMPLTEYL	201	
Db	583	EKLIDPVTSDRESKPKSPAKKAPAPADTKPAEAEVPEEHEYCDMLCKCFKRPWKKY-	641	
Qy	202	KRIKLPNSIDSYTDRLLYLLMLLLVTLAYNNCWFIPLRLVPPYQTDANIHWLLADIICD	261	
Db	642	---QFQOSIDPLTNLMYLVLMFFVVMAWNNCWLIPIVRWAPFYQTPONIHHWLLMDLYCD	698	
Qy	262	IIVLYDMLFITQRLQFVRGGDIIIVDSNELRKHYRTSTKFDLDVASIIPFDICYLFFGFNP	321	
Db	699	LIYFLDITVQTRLQFVRGGDIITDKDMRNNYLKSRFXKMDLLSLPLDLYLKVGWNP	758	
Qy	322	MFRANRMLKTSFPFENHLESIMDKAYIVRVIRTTGYLLFILHINACVYVWASNYEGIG	381	
Db	759	LLRLPRLCKYMAPEFNFESRLSLSKAYVYRVIRTTAYLLYSHLNCLYVWASAYQGLG	818	
Qy	382	TTRVYDQEGNEYLURCYVWAVRTLITIGGLPEPOTLFEIVQLLNFFSGVVFSSLLGQM	441	
Db	819	STHWYDQVGNYSYRCYFAVKTLITIGGLPDPKTLFEIVQLLNYYTGVFAFSVMLGQM	878	
Qy	442	RDVIGAATANQNYPRACMDDTIAYMNNYSIPKLVOKRVRTWYEVTWDSQRMLESDDLKT	501	
Db	879	RDVVGAAATAGTYYRSCMDSTVKYMNFKYIPKSVQNRVKTWYEVYTHWSQGMLESSELMVQ	938	
Qy	502	LPITTVQLALADVNFSIISKVDLPKGCDDTOMIDMLLRKLSVLYLPDGFVCKKGEIGKEM	561	
Db	939	LPDKRRLDLADVNINIVSKVALPFGQCDROMIFDMLKRLRSVVLYPNDIVCVCKGEIGREM	998	
Qy	562	YIIKHGEVQVLGGPDGTIKVLYTLKAGSVFGEISLLAAGGNRRRTANVVAHGFAKLLTLDK	621	
Db	999	YIIQAGVQVLGGPDGKSVLYTLKAGSVFGEISLLAAGGNRRRTANVVAHGFTWLLFLDK	1058	
Qy	622	KTLQELVHYHPPDSRILMKKARVLLKQAKTAETPPRKDLALLFPKPEETPKLFKTLIG	681	
Db	1059	KDLNEILVHYEPESQKLKFKKARMLRSNNK-----PKEEKSVLILPPRAGTPKLFNAALA	1113	
Qy	682	GTGKAS-----LARLLKLKREAAAKKENSBBGEEGKNEKDNEDKQKE	729	
Db	1114	MTGRMGKGKAGGKLAHLRLKELAALEAAKQOEL---VEQAKSDQVKGEEGSAAPD	1170	
Qy	730	NEDKQKE-NEDKDQGRSPEEKP-----LDRPECTASPIAEEEPHSVRTVLPR	777	

Qy	700	AQKENS	706	
	:	:	:	
Db	956	MRRKQS	962	
RESULT 12				
ABG05466	ABG05466 standard; protein; 644 AA.			
ID	AC	AC	AC	ABG05466;
XX	XX	XX	XX	13-FEB-2002 (first entry)
XX	XX	XX	XX	Novel human diagnostic protein #5457.
XX	XX	XX	XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	XX	XX	XX	food supplement; medical imaging; diagnostic; genetic disorder.
OS	XX	XX	XX	Homo sapiens.
XX	XX	XX	XX	WO200175067-A2.
XX	XX	XX	XX	11-OCT-2001.
XX	XX	XX	XX	30-MAR-2001; 2001WO-US008631.
XX	XX	XX	XX	31-MAR-2000; 2000US-00540217.
PR	XX	XX	XX	23-AUG-2000; 2000US-00649167.
XX	XX	XX	XX	(HYSE-) HYSEQ INC.
PA	XX	XX	XX	Drmanac RT, Liu C, Tang YT;
PI	XX	XX	XX	WPI; 2001-639362/73.
DR	XX	XX	XX	N-PSDB; AAS69653.
XX	XX	XX	XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	XX	XX	XX	diagnostics, forensics, gene mapping, identification of mutations
PT	XX	XX	XX	responsible for genetic disorders or other traits and to assess
PT	XX	XX	XX	biodiversity.
XX	XX	XX	XX	Claim 20; SEQ ID NO 35825; 103pp; English.
PS	XX	XX	XX	The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC	XX	XX	XX	sequences. (I) is useful as hybridisation probes, polymerase chain
CC	XX	XX	XX	reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC	XX	XX	XX	and in recombinant production of (II). The polynucleotides are also used
CC	XX	XX	XX	in diagnostics as expressed sequence tags for identifying expressed
CC	XX	XX	XX	genes. (I) is useful in gene therapy techniques to restore normal
CC	XX	XX	XX	activity of (II) or to treat disease states involving (II). (II) is
CC	XX	XX	XX	useful for generating antibodies against it, detecting or quantitating a
CC	XX	XX	XX	polypeptide in tissue, as molecular weight markers and as a food
CC	XX	XX	XX	supplement. (II) and its binding partners are useful in medical imaging
CC	XX	XX	XX	of sites expressing (II). (I) and (II) are useful for treating disorders
CC	XX	XX	XX	involving aberrant protein expression or biological activity. The
CC	XX	XX	XX	polypeptide and polynucleotide sequences have applications in
CC	XX	XX	XX	diagnostics, forensics, gene mapping, identification of mutations
CC	XX	XX	XX	responsible for genetic disorders or other traits to assess biodiversity
CC	XX	XX	XX	and to produce other types of data and products dependent on DNA and
CC	XX	XX	XX	amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC	XX	XX	XX	amino acid sequences of the invention. Note: The sequence data for this
CC	XX	XX	XX	parent did not appear in the printed specification, but was obtained in
CC	XX	XX	XX	electronic format directly from WIPO at
CC	XX	XX	XX	ftp.wipo.int/pub/published_pct_sequences
SQ	XX	XX	XX	Sequence 644 AA;
Query Match 25.7%; Score 1088; DB 4; Length 644;				
Best Local Similarity 100.0%; Pred. No. 2e-83;				
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
Qy	594	SLLAAGGNNRTANVVAHGFANLLTLDKTKTQELIVHPDSEIILMKARVLLKQAKTA	653	

Db	224	SFSPIWFVDCDDPNLTSVLRPEDTENNYYLRQOLKCTWFMFLDOPLPWGQNGKIEVTS	283
QY	303	-----	302
Db	284	EBEBEMAGDIKYLNHCKWKKEELISGKKLEDEGIEKENLATLEKIRKTSQGHNLNVMKC	343
QY	303	-----	302
Db	344	LGSGETTKPRNSGSTRRKESKQLKAGSQREWLVQIQTIGILMSEKAEIWTALYYTQHA	403
QY	303	-----DVASITPF-----	310
Db	404	ARQFEGESKDLASCLQYSRWVDNEGSLNREQEERLLELEQKAEIWEQVEVHRQTL	463
QY	311	-----DICVLPFGFNPMPFRANRMLKYTSFFP-----	336
Db	464	TMQNDLTTTISHAVFONGELKEQLAKLQTGFPMKLNENWEITSTPQSEOHKKKEPSEKLG	523
QY	337	-----FNH	339
Db	524	GLDSEELPLMPSIPEELESREAMVAFUNSAVASAEEOAWPRQLKEQKGAMEKLQSH	583
QY	340	HLESTMCKAYIYR-----	352
Db	584	FMELMOEKVDLKEOMEKLERRCIQLSGETDVIHHTVPELEVSADVAPEGIHQPFPGQ	643
QY	353	-----	352
Db	644	GDGEAGAAGAAGAAGGIPERGIVIGNDSSTHVMPEDLPGQDVEDSDIDDP	703
QY	353	---VIRTTGYLLFILHINACVYTMASNYEGIGTTRWVYDGEENE	393
Db	704	DPVIRTGYLLFILHINACVYTMASNYEGIGTTRWVYDGEENE	747

RESULT 15

ABR39396

ID ABR39396 standard; protein; 237 AA.

XX ABR39396;

XX

XX

DT 26-JUN-2003 (first entry)

XX

DE Amino acid sequence of human beta1b.

XX

KW OCN1; OCN2; beta1b; CNG; human;

KW olfactory cyclic nucleotide gated channel subunit.

XX

OS Homo sapiens.

XX

XX WO2003004611-A2.

PN

PD 16-JAN-2003.

PP

PF 08-JUL-2002; 2002WO-US021184.

XX

PR 06-JUL-2001; 2001US-0303140P.

PR 10-DEC-2001; 2001US-0337154P.

XX

XX

PA (SENO-) SENOMYX INC.

XX

XX Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JE;

PI Servant G, Callamaras N;

PI

XX WPI; 2003-229406/22.

DR

DR N-PSDB; ABZ80565.

XX

XX

PT Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b

PT olfactory cyclic nucleotide gated (CNG) channel subunits, useful for

PT identifying the CNG channel activators useful for enhancing smell.

XX

PS Disclosure; Page 86; 97pp; English.

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 21, 2005, 19:47:49 ; Search time 43 Seconds

(without alignments)
1810.218 Million cell updates/sec

Title: US-09-855-828-1

Perfect score: 4234

Sequence: 1 MFKSLTKVKKVPDIGNENN.....PSABGGEEVLTIIEVKEKAKQ 809

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1952	46.1	909	2 S32538	CGMP-gated cation
2	1095	25.9	800	2 T19627	hypothetical prote
3	834.5	19.7	695	2 S74179	cyclic nucleotide-
4	829	19.6	663	2 S11521	CAMP-gated channel
5	821.5	19.4	735	2 I50630	alpha subunit of c
6	820	19.4	732	2 S35691	cyclic nucleotide-
7	819.5	19.4	688	2 B42161	CGMP-gated cation
8	818.5	19.3	690	2 A42161	CGMP-gated cation
9	818	19.3	685	1 A44842	CGMP-gated ion cha
10	807.5	19.1	682	1 JH0550	cyclic nucleotide-
11	804	19.0	664	2 T11517	cyclic nucleotide-
12	801.5	18.9	691	2 J06509	rod cyclic nucleot
13	797	18.8	690	1 S07103	CGMP-gated ion cha
14	794	18.8	706	2 A55251	cyclic nucleotide-
15	771	18.2	645	2 I50680	alpha subunit of r
16	770	18.2	772	2 S28232	hypothetical prote
17	718	17.0	665	2 S52072	DmCNGC protein - f
18	640	15.1	575	2 I59327	olfactory cyclic n
19	550	13.1	673	2 T20936	hypothetical prote
20	535	12.5	611	2 T20935	hypothetical prote
21	484	11.4	261	2 I78559	cyclic nucleotide-
22	476	11.2	261	2 I78560	cyclic nucleotide-
23	441.5	10.4	644	2 T33125	hypothetical prote
24	366.5	8.7	767	2 T21969	hypothetical prote
25	349	8.2	828	2 T52046	potassium channel
26	349	8.2	962	2 I53197	potassium channel
27	336	7.9	989	2 I48912	potassium channel
28	331.5	7.8	807	2 T12177	potassium channel
29	323.5	7.6	845	2 T07052	probable potassium

30	321	7.6	688	2 S55349	potassium channel
31	318	7.5	787	2 S68699	potassium channel
32	317.5	7.5	1159	2 I38465	probable potassium
33	314	7.4	883	2 T07651	potassium channel
34	313.5	7.4	662	2 T04461	potassium channel
35	311	7.3	887	2 T03939	potassium channel
36	302.5	7.1	838	2 S23606	potassium channel
37	302.5	7.1	857	2 S62694	potassium channel
38	296	7.0	934	2 T42394	potassium channel
39	292	6.9	1174	2 A40853	potassium channel
40	287	6.8	716	2 T51354	cyclic nucleotide-
41	284	6.7	706	2 T51432	cyclic nucleotide-
42	282	6.7	880	2 F85381	potassium channel
43	282	6.7	916	2 T05360	probable potassium
44	280	6.6	702	2 T04424	probable calmoduli
45	278.5	6.6	718	2 G84902	hypothetical prote

ALIGNMENTS

RESULT 1

S32538

CGMP-gated cation channel 2, rod - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004

C;Accession: S32538

R;Chen, T.Y.; Peng, Y.W.; Dhallan, R.S.; Ahmed, B.; Reed, R.R.; Yau, K.W.

Nature 362, 764-767, 1993

A;Title: A new subunit of the cyclic nucleotide-gated cation channel in retinal rods.

A;Reference number: S32538; MUID:93226050; PMID:7682292

A;Accession: S32538

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-909 <CHE>

A;Cross-references: UNIPROT:O43636; UNIPARC:UPI000017C0CA

C;Keywords: CGMP binding

F;620-742/Domain: CAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 46.1%; Score 1952; DB 2; Length 909;

Best Local Similarity 46.4%; Pred. No. 2.3e-113;

Matches 405; Conservative 121; Mismatches 237; Indels 110; Gaps 18;

Qy	14	IGENNENEOSSRRNEGSHPSNQSQQTTAQE	---ENKGE---	EKSLTKTSPTVTSERPHTN	68
Db	67	VGEAKKEAEKAEAEVAEEAEAEKEPDMAETKEEPEAEAEAAASSGVPATKQHPEVQ	126		
Qy	69	IQDK-----LSKXSSSGDLTTNPDQNAAEPTGTVPQEKMDPGKEGN	-----	112	
Db	127	VEDTDADSCPLMAEENPPS--TVLPPSPAKSDTLIVPSSASGTHRKKLPSDEDEAEELK	184		
Qy	113	--SPQNKP-----PAAP-----VINEYADAQLHNLVKRMWRORTALY	146		
Db	185	ALSPAESPVVAMSDPTTPKDTGDQDRAASTASTNSAIIND---	RLQELVKLPKTEKV	240	
Qy	147	KXKLVEGDLS-----SPEASQTAKPATVPPVKESDDKPT--EHYRLLWFKVKKMPLEY	200		
Db	241	KEKLIDPDVTSDEESPSPAKKAPAPDTPKPAEAPVEEHCYDMCLCKFKRHPWKY	300		
Qy	201	LKRILKPNSTDSYTDRLYLWLLVLAYNMCWFILRLVFPYOTADNLHYMLADIIC	260		
Db	301	----QFPOSIDPLTNLMYLVWLFVVMWNNCWMLIPRWAFPVOTPDNIHMLLMYDLC	356		
Qy	261	DIIVLYDMLFIQRLQFVRGDDIIVDSNELRKHYRTSTKFDQVASTIIPEDICVLYFFGN	320		
Db	357	DLIVFLDITVFQRLQFVRGDDIITDKDMNNYKSRREPKMDLLSLPLDFLYLKGVN	416		
Qy	321	PMFRANMLKYTSFFPFNNHLESIMDKAYIYRVIRTTGYLLFILHINACVYVWASNYEGI	380		
Db	417	PLLRPLRCLKYMAPPFENSRLESILSKAYYVYRVIRTTAYLLYSLHLSCLYVWASAYOGL	476		
Qy	381	GTTRWVYDGGENLYLCRYWAVRTLITIGGLPEPQTLFEIVFOLLNFFSGVVFSSLIQ	440		

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Db 477 GSTHWYDVGNSYRCYYFAVKTLITIGGLDDPKTLFBIVFQLNMYFTGVFAFSWIMQ 536
Qy 441 MRDVGAAATANQNYFRACDDTIAYNNYSIPKLQKRVRTWYEYTWDSQRMLEDSDLK 500
Db 537 MRDVVGAAATAGQTYRSCNDSTVKYWNFYKIPKSVQNRVKTWYEYTWHSQGLDSELMV 596
Qy 501 TLPSTVQLALADVNPISIISKVDLPKGGCDTQMIYMLLKLKSVLYLPDGFVCKKGIGKE 560
Db 597 QLPDRKMLDLADVNNYINISKVALFQCDQRMIFDMLKELRSVYLPNDYVCKKGIGRE 656
Qy 561 MYIIKHGEVQVLGGDGTGVLVTLKAGSVFGEISLLAAGGNRRRTANVAHGFANLLTLD 620
Db 657 MYIIQAGQVQLGGPDGKSVLTLKAGSVFGEISLLAAGGNRRRTANVAHGFANLLTLD 716
Qy 621 KKTLOEILVHYDPDSERILMKKARVLLKOKATAEATPPRKDLALLFPKPEETPKLPKTL 680
Db 717 KKDLEILVHYDPESOKLLRKARRMLRSNNK-----PKEEKSVLLLPAGGATPKLPFNAAL 771
Qy 681 GGTGKAS-----LALLKLRQAAQAKKENSEGGEENKEDKOKEDKOK 728
Db 772 AMTGRMGKGKAGKGLAHLARLRLKELAALEAAKQOEL---VEQAKSSQDVKGEESAAP 828
Qy 729 ENEDKGS-NEBKDGREPEKP-----LDREPTASPTAVEEPEHSHSVRTVLP 776
Db 829 DQHTPKAEATDPPAPRTPEPPGSPSPPPASLGRPEGBEIPA-EPEHSHSV-----882
Qy 777 RGTSRQSLIISMAPSAEGGEVLTIEVKEKAG 809
Db 883 -----ICMSGPEPEGEQILSVKMPERE 906

RESULT 2
T19627
hypothetical protein F36F2.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T19627; T21863
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19627
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-800 <WIL>
A:Cross-references: UNIPROT:O622237; UNIPARC:UPI0000083D03; EMBL:Z93778; PIDN:CAB07847.1;
A:Experimental source: clone C31H5
R:Cottage, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19479
A:Accession: T21863
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-800 <W12>
A:Cross-references: UNIPARC:UPI0000083D03; EMBL:Z81532; PIDN:CAB04328.1; GSPDB:GN000019;
A:Experimental source: clone F36F2
C:Genetics:
A:Gene: CESP:F36F2.5
A:Map position: 1
A:Introns: 27/3; 51/2; 142/2; 191/3; 287/3; 333/3; 355/2; 405/1; 433/2; 484/1; 508/1; 56

Query Match 25.9%; Score 1095; DB 2; Length 800;
Best Local Similarity 31.9%; Pred. No. 3.4e-60;
Matches 258; Conservative 153; Mismatches 301; Indels 98; Gaps 22;

Qy 2 FKSLLTKVNVKPIGENENNEQSSRRNEEG---SHPSNQSQQTAAQENKGEKSUKTKST 58
Db 21 PSYDRQKASKPT-QLSEKWKSPRSDSFLLDPANAS-----KPSASTRL 68
Qy 59 PV-TSEEPHTNIQDKLSKKNSSGDLITNP-----DPQNAAEPTGTVPQEKMDPGKEGN 112
Db 69 PYPTRPPEVVIQI-----DEVESFILGLIDETDDELGD-----RLDPASSFDA 113
Qy 113 SPQNPAPPAAPVINEYADAO-----LHNVKRMQRQRTALYKKKLVLGEGDLSSEASPT 164
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Db 114 NLSATRASSIIEDVRSQISPIMRERLHSAKEVHRRTSAVREDLIR---ETPEDTVSM 170
Qy 165 AKPTAVPPVKSGDDKPTHEHYRLWFKVK-KMPLTEYLKR---IKLPNSIDSYTORLYLL 220
Db 171 A--SNVP--KONEHRPS--LMSLIGLQNRSESPVDTVKNCFGFSKGTFFHPY-GRFYMT 223
Qy 221 WLLLVTLAYNNWCWPIPLRLVFPYQYQADNIHLYLIADIICDIIYLYDMFLIPRIQFVRG 280
Db 224 WLSLVTLCFLFNACFIPLRSSYPYQYQADNIHLYLIADIICDIIYLYDMFLIPRIQFVRG 283
Qy 281 GDIIVDSNELKHYRTSTKFDVASIIPDICYLFFGFGNPMFRANRMLKYTSFEFNNH 340
Db 284 GIQVXIYKDTORHYLMTRTFKLDILSLTDLMTLWYFFGKMPITWIRNRLKNSPFLFDM 343
Qy 341 LESIMDKAVIVRVTRTGYLFIHLINACVYVYASNYEGIG-----TTTWWVVDG 389
Db 344 LNSFANPYAIRIAKTLSTMIYIHCNSCVYKUSALQAFQAIYLENGKMYLKNWVYNN 403
Qy 390 EGNELRCVYMAVRLTITIGGLPEPOTLFEIVFOLLNFFSGVFPSSLIGOMRUVIGAT 444
Db 404 QGNAYIRCFYPTAAVATSTGNPAPTNNVIEIYMTCSMMMGVVFALLLLGOIRDIVSNAN 463
Qy 450 ANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYEYTWDSORMLDESOLLKTLPTTVQLA 509
Db 464 RNREEFORMDLALGECKKLGLKMETTNRVRDWFYITWQOQKTLDEKKLIEKLPILQTD 523
Qy 510 LAIDVNFISIISKVDLPKGGCDTQMIYMLLKLKSVLYLPDGFVCKKGIGKEKMYIHKHGFV 569
Db 524 LALSVMHTTSLSKVQLFQCDRALRLDLVLRPVIFLPGDMICLKGDVGKEMYINQGLI 583
Qy 570 QVLGGPDGTVLTLKAGSVFGEISLLAAGGNRRRTANVAHGFANLLTLOKKTQEIILV 629
Db 584 QVVGSDHNEKIFAEALQAQAVFGEISLLAAGGNRRRTASIRAKGYCTLFVLAKEDLNDVIR 643
Qy 630 HYPDSERILMKARVLLKQAKTAEATPPRKDLALL-----FPPKEETPKLPKTLGGT 683
Db 644 YYPQAQTLIRKKAAMLKNDKSKDEKTEKIKAQAELEDRCCKINPR-QVPKLITLIANMTE 702
Qy 684 -----GKASLARLLKLKREAAQKK-----ENSEGGEENKEDKOKENED 729
Db 703 MNENKGVQELKKVIEEETEKRRRSIYYPWSTLQRDDDEBEWDEEDLSOVGEDFDLDP 762
Qy 726 -KQENKGVQELKKVIEEETEKRRRSIYYPWSTLQRDDDEBEWDEEDLSOVGEDFDLDP 754
Db 763 TNHSDDED---PMEDVDLAPVHDDDDWQDP 789

RESULT 3
S74179
cyclic nucleotide-gated channel protein - human
C:Species: Homo sapiens (man)
C>Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 16-Jul-1999
C:Accession: S74179
R:Yu, W.P.; Grunwald, M.E.; Yau, K.W.
FEBS Lett. 393, 211-215, 1996
A:Title: Molecular cloning, functional expression and chromosomal localization of a human
A:Reference number: S74179; MUID:96400910; PMID:8814292
A:Accession: S74179
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-695 <YUW>
A:Cross-references: UNIPARC:UPI00000177899
A:Experimental source: retina
C:Genetics:
A:Map position: 2
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-gated
C:Keywords: ion channel; ion transport; membrane protein
F:482-607/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology (CA)
Query Match 19.7%; Score 834.5; DB 2; Length 695;
Best Local Similarity 29.7%; Pred. No. 4.3e-44;
Matches 223; Conservative 149; Mismatches 271; Indels 107; Gaps 22.
```



```

Db      3  LSKMTNINIWMSFVNPVNPVPALEKEIRRMWENGACSFSDDDN-----GSLSESENE 57
Qy      106 PG-----KEGPNSPQNKPPAAPV---INAYADAQLHNLVKRMQRORTALYKXKGLVEGD 154
Db      58  DSFFRSNSYKRRGSPQREQHLPGCTWALFNVNSSNKKQEPKPKKKKK-----EKSKADD 113
Qy      155 LSPSPASPTAKTAVPPVKESDDKPTTEHYHLLMFKVKKMPLELYLKRKIKLPNSIDSYT 214
Db      114 KNEKNKDPKPKKKKE-----KKEKKKKKE-----KKEKKKEEKKVVVVDPSGNTYY 162
Qy      215 DRLYLMLLLVTL--AYNNCNWFILPLRVPYQTDNIHYWLIADIICDIIVLYDMLFIQ 272
Db      163 N-----WLFCTITLFWNWT--MIARACFDELQSDVLYLFIQVSNVYIADM-FVR 214
Qy      273 PRLQFVRGDDIIVDSNELKRYRTSTKFDLVASIIIPDICYLFFGFN-PMFRANRMLKY 331
Db      215 TRTGYLEQGLLVKORMKLEIKYKANLQFKLDVLSVPTDLLYIKFGWNYPEIRLNRLAI 274
Qy      332 TSFFFNHLESIMDKAYIRVIRTTGYLLFILHINACVYVWASNYEGIGTTRVY----387
Db      275 SRMFEPFOTRTNYPNIFRISNLVMYVIIHWNACVYYSISKAIGFGNDTWVYPDVN 334
Qy      388 DGE-----GNEYLECYVWARTLITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMRD 443
Db      335 DPEFGRLARKYVYSLWSTLTITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMRD 394
Qy      444 VIGAAATANQNYFRACMDTIAYNNYSIPKLQKRVRTWYETWDSQRMLESLLKTLIP 503
Db      395 MTSNNNAARAEFGSRVDAIKQYMNFRNVSKDMKRVIKWFDYLTWTKTVDREVLRYLP 454
Qy      504 TTVQLALAIQVNSIISKVDFKGCOTQMIYDMLLKLKSVLYLPQGVCKKGIGKEMYI 563
Db      455 DKLRABIAINVHLDTLKKRIFADCEAGLLVELVLKLPQVYSPGYICKKGIGREMYI 514
Qy      564 IKHGEVQVGLPGGTQVLYTLKAGSVGEISLLAAG--GNRRTANVAHGAFANLLTLD 620
Db      515 IKEGKLAV-ADGGITQFVVLSDGYSFGEISILNKGKAGNRRTANIKSIGYSDFCLUS 573
Qy      621 KKTQILVHYPDSEIRILMKKARVLL 646
Db      574 KDDLMEVLYEPDAKTMLBEKGRQIL 599

RESULT 8
A42161
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A42161
R;Pittler, S.J.; Lee, A.K.; Alther, M.R.; Howard, T.A.; Seidlin, M.F.; Hurwitz, R.L.; Wa
J. Biol. Chem. 267, 6257-6262, 1992
A;Title: Primary structure and chromosomal localization of human and mouse rod photorece
A;Reference number: A42161; MUID:92210603; PMID:1372902
A;Accession: A42161
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-690 <PT>
A;Cross-references: UNIPROT:P29973; UNIPARC:UPI0000163B2A; CB:MB4741; NID:q180461; PIDN:
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C;Keywords: cAMP binding; transmembrane protein
F;479-603/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.3%; Score 818.5; DB 2; Length 690;
Best Local Similarity 30.08; Pred. No. 4.2e-43;
Matches 221; Conservative 126; Mismatches 262; Indels 125; Gaps 22;

Qy      5  LTKVNVKPKICGNNENQSSRRNEEGSHPS-----NQSQQTAAQENKGE-----KSL 53
Db      17  VTMPNVIVP-----DIEKIRRMWENGACSFSDDDDSAYTSESENENPHARGSFYSKSL 71
Qy      54  KTKSTPTVTSSEPHNTIQQKLSKNSSGDLTTNPPQNAAPTGTVPQKEMDPKSGPNS 113

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Db      72  R-KGQPSQREQVLPGLAI FNVNNS-----NKD-----QEPEKKKKKKKKSKSDKNE 121
Qy      114  POKPAPAPVINEYADAQLHNLVKRMQRORTALYKXKGLVEGDLSSPEASPTAKTAVPPV 173
Db      122  NKNDPE-----KKKKKKKKKK-----E 141
Qy      174  KESDDKPTTEHYHLLMFKVKKMPLELYLKRKIKLPNSIDSYDRLYLMLLLVTL--AYNW 231
Db      142  EKSKDKKHH-----KKEVVV-----IDP-SGNTYYNWLFCITLPMVYWN 180
Qy      232  NCWFILRLVFPYQTDNIHYWLIADIICDIIVLYDMLFIQPRLOFVRGDDIIVDSNELR 291
Db      181  T--MYIARACFDELQSDVLYLFIQVSNVYIADM-FVTRTGYLEOGLLVKELKLI 237
Qy      292  KHYRTSTKFDLVASIIIPDICYLFFGFN-PMFRANRMLKYTSFFFNHLESIMDKAYI 350
Db      238  NKYKSNLQFKLDVLSVPTDLLYIKFGWNYPEIRLNRLRFRSMFEFFORTTETRTNYPNI 297
Qy      351  YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRVY----DGE-----GNEYLECYVWAV 402
Db      298  FRISNLVMYVIIHWNACVYYSISKAIGFGNDTWVYPDINDEPFGRLARKYVYSLWST 357
Qy      403  RLTITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIQOMRDVIGAAATANQNYFRACMDDT 462
Db      358  LTLTIGETPPVRDSEYVVFVDFLIGVLIFATIVGNIGSMISNNNAARAEFOARIDA 417
Qy      463  IAYMNNYSIPKLQKRVRTWYETWDSQRMLESLLKTLPTTVQJLALAIQVNSIISKV 522
Db      418  KQYMHFRNVSKDMKRVIKWFDYLTWTKTVDREVLRYLP 477
Qy      523  DLFPKGCOTQMIYDMLLKLKSVLYLPQGVCKKGIGKEMYI IKHGEVQVGLPGGTQVLY 582
Db      478  RIFADCEAGLLVELVLKLPQVYSPGYICKKGIGREMYI IKEGKLAV-ADGGITQFV 536
Qy      583  TLKAGSVGEISLLAAG--GNRRTANVAHGAFANLLTLDKKTQLQEIIVHYVPSIRILM 639
Db      537  VLSGDSFTFGEISILNKGKAGNRRTANIKSIGYSDFCLSKDDLMLEALTEYDPAKTML 596
Qy      640  KKARVLLKKA-----KTAETATPRKDLALFPPEKEETPKLFTKLLGGTGKASLARLL--- 692
Db      597  EKGKQILMKDGLDLNLINAGSDPKDLBEKVTMEGSDVLLQ-----RPARILAEY 648
Qy      693  -----KLKREQAQKK 703
Db      649  ESMQKQLKQRLTKVEK 664

RESULT 9
A44842
C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A44842
R;Dhallian, R.S.; Macke, J.P.; Eddy, R.L.; Shows, T.B.; Reed, R.R.; Yau, K.W.; Nachans, J
J. Neurosci. 12, 3248-3256, 1992
A;Title: Human rod photoreceptor cGMP-gated channel: amino acid sequence, gene structure
A;Reference number: A44842; MUID:92356211; PMID:1379636
A;Accession: A44842
A;Molecule type: mRNA
A;Residues: 1-686 <DHA>
A;Cross-references: UNIPARC:UPI000008787; GB:942457; NID:9252853; PIDN:AB22778.1; PID:
A;Experimental source: retina
A;Note: sequence extracted from NCBI backbone (NCBIN:110250, NCBIP:110251)
C;Keywords: cAMP binding; eye; ion channel; ion transport; retina; transmembrane protein
F;475-599/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

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Query Match 19.3%; Score 818; DB 1; Length 686;
Best Local Similarity 29.9%; Pred. No. 4.4e-43;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

QY 5 LTKVNVKPIGENNENEGSSRRNEGSHPS-----NQSQTTAEENKGBE-----KSL 53
DB 13 VTMPNVIVP-----DIEKEIRMERGACSSFSFEDDSASTSESENPHARGFSYKSL 67
QY 54 KTKSPFVTSSEPHNTIQDKLSKKNSSGDLTTPNPDQNAAEPTGTVPQEKMEPGKGGNS 113
DB 68 R-KGSPSREQVLPAGIALFVNNS-----NKD-----QEPKKKKKKKKKSKDNKKE 117
QY 114 POKKPAAPVINEYADAQLHNLVKRMQRORTALYKKLVVEGDLSSPEASQTAKTAVPPV 173
DB 118 NKNDPE-----KKKKKKKKKKK-----E 137
QY 174 KESDDKPTHEHYRLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYLWLLVLT--AYNW 231
DB 138 EKSDDKKEE-----KKEVV-----IDP-SGNTYNNLFCITLPMVMNW 176
QY 232 NCWFTPLRLVFPYQTADNIHYWLIADIICDIILYDMLFIQRLQFVRGGDIIVDSNELR 291
DB 177 T--WVIARACFDELQSDYLEWLLDYSDIVLIDM-FVTRTGYLEQLLVKELKLI 233
QY 292 KHYRTSTKQOLDVASIIPDICYLFFGFN-PMFRANRMLKYTSFPEFNHHLESIMDKAYI 350
DB 234 NKYKSNLQPKLDVLSIPTDLLYFKLGWNPYPIRLNRLRFRSMFEFFORTETRTNYPNI 293
QY 351 YRVIRTTGYLLFIHINACVYVWASNYEGIGTRWY-----DGE-----GNEYLRCYNAV 402
DB 294 FRISNLVMYIVIIHWNACVFYSISKAIGFGNDTWYDINDPFRGLARKYVYSLYNST 353
QY 403 RLTIITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIGQMRDVGAAATANONYFRACMDT 462
DB 354 LTLTIGETPPVRSEYVVFVVDLGLVLI FATIVGNIGSMISNMNARAEPQARIDAI 413
QY 463 IAYMNYSIPLKVKRVRTWYBYTWSQRMDESLLKTLPTTVQALAIADVNFISIISKV 522
DB 414 KQYMHFRNVSKMEKRVIKWFDYLTWTKTVDKEVLKYLDPKRAEIAINVHLDLTKKV 473
QY 523 DLFKGCDDTQMIYDMLRLKSVLYLPGDFVCKKEIGKEMYIIKHGEVOVLGGPDGTVLV 582
DB 474 RIFQDCEAGLVVELVLRPQVYSPGDYICKGDIKREMYIIKEGQAVV-ADGGVTOFA 532
QY 583 TLKAGSVFGEISLLAAGG---GNRRATANVAHGFANLLTLDKKTQLQEILVHPDSEIIM 639
DB 533 VLSDSYFGEISILNIKSGKAGNRRTANIKSIGSDLFCLSKDDLMEALTEYDPDAKTMLE 592
QY 640 KQARVLLKQKA-----KTAEATPPKDLALLFPKKEETPKLFTKLLGGTKASLARLL--- 692
DB 593 EKGQILMKDGLLDLNIANAGSDPKLEBKVTRMEGSDVLLQT-----RPARILAEY 644
QY 693 -----KLKREQAOKK-----ENSEG-GESEG 713
DB 645 ESMQOKLQKRLTKVEKFLKPLIDTFSSIEGPGAESG 681

RESULT 10
JH0560
cyclic nucleotide-gated channel - channel catfish
C:Species: ictalurus punctatus (channel catfish)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: JH0560
R:Goulding, B.H.; Ngai, J.; Kramer, R.H.; Colicos, S.; Axel, R.; Siegelbaum, S.A.; Chesne
Neuron 8 45-58, 1992
A>Title: Molecular cloning and single-channel properties of the cyclic nucleotide-gated
A:Reference number: JH0560; MUID:92110008; PMID:1370374
A:Accession: JH0560
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-682 <GOU>
A:Cross-references: UNIPROT:P55934; UNIPARC:UPI0000127C25; GB:M83111

A:Experimental source: olfactory epithelium
C:Comment: This cyclic nucleotide-gated channel is activated equally well by both cAMP and
C:Superfamily: cyclic nucleotide-gated channel; cAMP binding; ion channel; ion transport; olfaction; transmembrane
C:Keywords: cAMP binding; cGMP binding; ion channel; ion transport; olfaction; transmembrane
F:137-157/Domain: transmembrane #status predicted <TS1>
F:173-193/Domain: transmembrane #status predicted <TS2>
F:217-236/Domain: transmembrane #status predicted <TS3>
F:241-261/Domain: transmembrane #status predicted <TS4>
F:277-297/Domain: transmembrane #status predicted <TS5>
F:319-337/Domain: transmembrane #status predicted <TS6>
F:350-370/Domain: transmembrane #status predicted <TS6>
F:447-571/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 19.1%; Score 807.5; DB 1; Length 682;
Best Local Similarity 29.0%; Pred. No. 2e-42;
Matches 192; Conservative 137; Mismatches 256; Indels 77; Gaps 17;

QY 119 PAAPVINEYAD-----AQLHNLVKRMQRORTALYKKLVVEGDLSSPEA-----SPOTAKPT 168
DB 55 PSAEMLEAFTQRRPLARLVNLVLSUREWA---HKSLSVETE-QRPDSFLERPRGPOAANDQ 110
QY 169 AVPPVKESDDKPTHEHYRLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYLWLLVLTIA 228
DB 111 SAAPA-----DAPKTF-----KERWEGFVVSQSDDIYYWLFIALA 148
QY 229 --YNNMCWFILRLVFPYQTADNIHYWLIADIICDIILYDMLFIQRLQFVRGGDIIVD 286
DB 149 SLYNW--IMLVARACFDQLQDENFFLWGLDVLCDVIVLDTCLRLKTYGLEQLLVKLI 205
QY 287 SNELKHYRTSTKQOLDVASIIPDICYLFFGFNPMFRANRMLKYTSFPEFNHHLESIMD 446
DB 206 LAKLRDNYIRTLOPKLDFLSILPTTELLFFVTGYVQPLRFNRLRFRSMFEFFDRTETRN 265
QY 347 KAYIVRVIRTTGYLLFIHINACVYVWASNYEGIGTRWYVDGEGNE---YLRCYNAV 402
DB 266 YNAPRINCLILYLVIIHWNACIYAIKALGSSDTWYVSGONKTLSCFVVCYFYWST 325
QY 403 RLTIITIGLPEPQTLFEIVFOLLNFFSGVVFSSLIGQMRDVGAAATANONYFRACMDT 462
DB 326 LTLTIGEMPPPVKDEEYVVFVDFLVGLVIFATIVGNVGMIANMNATRAEFQTRIDAI 385
QY 463 IAYMNYSIPLKVKRVRTWYBYTWSQRMDESLLKTLPTTVQALAIADVNFISIISKV 522
DB 386 KQYMHFRNVSKMEKRVIKWFDYLTWTKTVDKEVLKYLDPKRAEIAINVHLDLTKKV 445
QY 523 DLFKGCDDTQMIYDMLRLKSVLYLPGDFVCKKEIGKEMYIIKHGEVOVLGGPDGTVLV 582
DB 446 RIFQDCEAGLVVELVLRPQVYSPGDYICKGDIKREMYIIKEGQAVV-ADGGVTOFA 504
QY 583 TLKAGSVFGEISLLAAGG---GNRRATANVAHGFANLLTLDKKTQLQEILVHPDSEIIM 639
DB 505 LLTAGCGFGEISILNIQSGKMGNRRTANIRSIGYSDLFCLSKDDLMEAAVEAPDAQKVL 564
QY 640 KQARVLLKQKA-----KTAEATPPKDLALLFPKKEETPKLFTKLLGGTKASLARLL---GT 683
DB 565 ERGREILRKQGLLDESVAAGGLVIDTEBKVERLDASL-----DILQTRFARLLGEFTST 619
QY 684 GKASLARLLKREQA-----AQKKENSEGGEEG---KENEDKOKENEDKOKENEDK 736
DB 620 ORRLKQRTALERQLCHTGLGLLSDNEAGEHAGVPTHTHADIHAQPEHTRTSAETNSE 679
QY 737 NE 738
DB 680 EE 681

RESULT 11
S11517
cyclic nucleotide-activated channel protein - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C:Accession: S11517
R:Dhallan, R.S.; Yau, K.W.; Schrader, K.A.; Reed, R.R.

Nature 347, 184-187, 1990
A:Title: Primary structure and functional expression of a cyclic nucleotide-activated ch
A:Reference number: S11517; MUID:903701115; PMID:1697649
A:Accession: S11517
A:Molecule type: mRNA
A:Residues: 1-664 <DNA>
A:Cross-references: UNIPROT:Q00195; UNIPARC:UPT0000000CF3; GB:X55519; NID:G56791; PIDN:C
C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-
C:Keywords: transmembrane protein
F:456-580/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>
Query Match 19.0%; Score 804; DB 2; Length 664;
Best Local Similarity 29.8%; Pred. No. 3.1e-42; Indels 108; Gaps 22;
Matches 219; Conservative 126; Mismatches 286; Indels 108; Gaps 22;
QY 50 ESKLTKSTPVTSEEPHTNIQDKLSKNSGDLTTNPDQNAABPTGTVPQEQ---EMDP 106
DB 4 EKSNGVKSPPANN---HNHPPPSIKANGKDDHRAGSRPQSVAAADDTSPELQRLAEMDT 60
QY 107 GKEGPNSPQNPAPAVINNEYADAQLH-----NLVKMRQRTALYKKLVKVEGDLSSPE 159
DB 61 PRGRGGFQIRVLGVGIRDWANKNFREBEPDPSFLERFR-----GPE 104
QY 160 ASPTAKPTAVPVKESDDKPTHEYHLLVFKVKMPLTEYLKRIKLPNSIDSYTDRLYL 219
DB 105 LQVTHHQDDKGGKGGKTKKPFELF-----VLDPAGD-WYY 143
QY 220 LWLLLVTL--AYNWCWFIPLRLVFPYQTADNIHYWLIADIICDIILYDMLFIQRLQF 277
DB 144 RLWLVAMPVLYNW-CLLV-ARACFDLQRYFVWLVLDYFSDTYVIAD-LIIRLTGF 200
QY 278 VRGDIIVDSNEIRKHYRTSTKFDLVASIIIPDICYLFFGP-NPMFRANMLKYTSFPE 336
DB 201 LEQGLLVKDPKLRDNYIHTLPKLDVASIIPDILYFAVGIHSPEVRNRLHFARMPE 260
QY 337 FNHLESIMDKAYIRVIRTTGYLLFILHINACVYVWASNYEGITRWY----DGE-- 390
DB 261 FPORTETRTSYNIFRISNLVILYIIHWNACIYVSKISGFGVDVTWYVYNTDPEYG 320
QY 391 --GNEYLCYVYVAVRTLTITIGGLPEPOTLPEIYFQILNFFSGVVFSSLIQMRDVIGAA 448
DB 321 YLAREYIYCLYWSLTLTITIGETPPPVKDEYLVFIPDFLIGVLIIFATIVGVNVSIMNM 380
QY 449 TANQNYFRACMDDTIAYMNNYSIPKLQKRVRTYETWDSQRMDBSLLKLTPTTVQL 508
DB 381 NATRAEFOAKIDAVHYMQPRKYSKDEAKVIKWFYLTNKTVDREVLLKLPALRA 440
QY 509 ALAIDVNFYSISKVDLPKCDTQMIYDMLRLKSVLYLPDGFCKKGEIGKEMVIIKHGE 568
DB 441 EIAINVHLSTLKKVRIQDCEAGLLVELVKLRPQVPSGDYICRKGDIKEMVIIKEGK 500
QY 569 VQVLGGPDGKVLVTLKAGSVFGEISLLAAG--GNRRTANVVAHFANLLTLDKKTQL 625
DB 501 LAVV-ADGGVQVALLSAGSFGGEISILNKGWGNERTANIRSLGYSDLPCLSKDDL 559
QY 626 EILVHPDSEIRILMKKARVLKQAKTAE---ATPPRKDALLPKPKETPKLFTLLGG 682
DB 560 EAVTEYDPAKVLBERGREILMKEGLLDENEVAASMEVDV-----QEKLEQETNM--D 611
QY 683 TGKASLARLLKLKEQAQAKENSEGEGEERKENEDKQEN--EDKQENEDKQENEDK 740
DB 612 TLYTRFARLL-----AEYTGAAQKQKQIRITVLETRKQNH-----EDDYL 651
QY 741 DKGREPEKPLDRPECTAS 759
DB 652 SDG-----INTPEPTAA 663

RESULT 12

JC6509

rod cyclic nucleotide-gated cation channel protein alpha-chain - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C:Accession: JC6509

R:Veske, A.; Nilsson, S.E.G.; Gal, A.

Gene 202, 115-119, 1997

A:Title: Characterization of canine rod photoreceptor cAMP-gated cation channel alpha-sub

A:Reference number: JC6509; MUID:98087425; PMID:9427553

A:Accession: JC6509

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-691 <VES>

A:Cross-references: UNIPROT:Q28279; UNIPARC:UPI0000127C19; EMBL:X99914; NID:gl488571; PII

C:Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide

F:478-602/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>

Query Match 18.9%; Score 801.5; DB 2; Length 691;

Best Local Similarity 29.2%; Pred. No. 4.7e-42;

Matches 220; Conservative 136; Mismatches 286; Indels 112; Gaps 23;

QY 21 EOSSRRNEGSHPSNOSQOQTAAEENKNGEKSUKTKSTPVTSEEPHTNIQDKLSKKNSSG 80

DB 24 EKEIRRMENGARSS-----FSDDDDGDDSDASMFES---ENETPIA--RDSRNNSSORR 72

QY 81 DUTTNPDQNAABPTGTVPQEKEMDPGKEGPNSPQNPAPAVINNEYADAQLHNLVKMR 140

DB 73 D-----PSQRE-----QVLPGAIALFNVNSSNKEOEPEKK 104

QY 141 QRTALYKKLVKVEGDLSSPEASPTAKTAVPPVKESDDKPTHEYHLLVFKVKMPLTEY 200

DB 105 KKKK--EKSKSGDKNENKKSEKKKKK---KEKEKKNKEK-----GKDKK---EEE 150

QY 201 LKRIKLPNSIDSYTDRLYLLWLLVTL--AYNWCWFIPLRLVFPYQTADNIHYWLIADI 258

DB 151 KKEWV---IDP-AGNMYNWLFCITLPMYNYWT--MVIARACFDELOSDYLEWIIIFDY 204

QY 259 ICDIILYDMLFIQRLQFVRGDIIVDSNEIRKHYRTSTKFDLVASIIIPDICYLFFPG 318

DB 205 LSDIVYLLDM-FVTRTGYLEQGLLVREBAKLEIKYKSNLQPKLQFSLVIPTDLYFLKLG 263

QY 319 FN-PMFRANMLKYTSFPEFNHLESIMDKAYIRVIRTTGYLLFILHINACVYVWASNY 377

DB 264 WNYPEIRLNRLLRISRMFEFFQRTETRTNYPNIFRISNLVMIYIIVHWNACVYFSIKA 323

QY 378 EGITGTRWY---DGE---GNEYLCYVYVAVRTLTITIGGLPEPOTLPEIYFQILNFFS 429

DB 324 IGFNDTWYVDPVNDPEFQRLARKYVYSLYWSLTLTITIGETPPPVVDSEYVVFVDPLI 383

QY 430 GVVFSSLIQMRDVIGAAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTYETWDS 489

DB 384 GVLIIFATIVGVNVSIMNMNAARAEFOARIDAIKQYMHFRNVSKMEKRVIKWFDYLWN 443

QY 490 QRMLESDDLKLTPTTVQALADIVNFSIISKVDLPKCDTQMIYDMLRLKSVLYLPDGD 549

DB 444 KKTVDKELVKYLPDKLRAEIAINVHLDLTKKVRIFADCEAGLLVELVLKLOPQVSPGD 503

QY 550 FVCKKGEIGKEMVIIKHGEVOVLGGPDGKVLVTLKAGSVFGEISLLAAG--GNRRTA 606

DB 504 YICCKGDIGREMIYIKEGKLVV-ADGGITQFVVLSDGSYFGEISILNKGKAGNRRTA 562

QY 607 NVVAHFANLLTLDKKTQLQEIIVHPDSEIRILMKKARVLKOKA---KTAETATPPRKDL 662

DB 563 NIKSIGYSDLPCLSKDDLMEALTEYDPAKTMLEKQKQILMKDGLLDINIANAGSDPKDL 622

QY 663 ALLFPKPEETPKLFTLLGGTGKASLARLLKLKEQAQAKENSEGEGEERKENEDKQKE 722

DB 623 EEKVTMRGSDVLLQT-----RFAIIL-----AEYESMOOK 653

QY 723 NEDQKQENEDKQENEDK---KGREPEEKPLD 752

DB 654 LKORLTQKVERFLKPIIDTFPSALEGTGDSRPLD 687

RESULT 13

S07103

cGMP-gated ion channel protein - bovine

Job time : 47 secs

Qy	571	VLGGPDKTVLVTLKAGSVGEISLLAAGG--GNRRTANVAHGFANLLTLDKKTQLQEI	627
Db	548	VV-AEDGITQVVLGDSYFGEISILNIGKSGNRTANIRISIGYSDLFCLSKDDLMEA	606
Qy	628	LHYPDSEIRILMKAR-VLLKQK--AKTAEATPPRKDLALLPFPKPEETPKFKTLLGGT	683
Db	607	LTEYPEAKKALEEKGRIOLMKDNLIDELAKAGADPKDI-----EEKVEHLETSLSL	659
Qy	684	GKASLARLL-----KLKREQAQKKN	705
Db	660	-QTRFARLLAEYNATQMKVQRLSQLES	686
RESULT 15			
150680			
alpha subunit of rod photoreceptor CNG-channel - chicken			
C;Species: Gallus gallus (chicken)			
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004			
C;Accession: I50680			
R;Bonigk, W.; Altenhofen, W.; Muller, F.; Dose, A.; Illing, M.; Molday, R.S.; Kaupp, U.E			
Neuron 10, 865-877, 1993			
A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channels			
A;Reference number: I50630; MUID:93264082; PMID:7684234			
A;Accession: I50680			
A;Status: preliminary; translated from GB/EMBL/DBJ			
A;Molecule type: mRNA			
A;Residues: 1-645 <BON>			
A;Cross-references: UNIPROT:Q90980; UNIPARC:UPI0000127C21; EMBL:X89599; NID:908852; PID			
C;Superfamily: cyclic nucleotide-gated channel; cAMP receptor protein cyclic nucleotide-			
P;431-555/Domain: cAMP receptor protein cyclic nucleotide-binding domain homology <CAP>			
Query Match 18.2%; Score 771; DB 2; Length 645;			
Best Local Similarity 34.3%; Pred. No. 3.4e-40;			
Matches 173; Conservative 104; Mismatches 196; Indels 32; Gaps 12;			
Qy	217	LYLLMLLLVTL--AYNNCNFIPRLVFPYQTDNIHLYLIADIIYLYDMLFIOPR	274
Db	116	MYNWLFCITPVMYNT--MIARACDFELQNDYLAWFIVDVSDVIYADM-FVTR	172
Qy	275	LQFVRGGDIIIVDSNELKRYRTSTKQLDVASIIIPDICYLFFGFN-PMFRANMLKYTS	333
Db	173	TGYLEQGLLVKEEQKLAKYKSSIQFKLDFLSIIPTDLLYFKLGNYPELRINRLVAR	232
Qy	334	PFPNHHLESIMDKAYIYRVRTTGYLLFLHINACYVWASNYEGIGTRWYVDGEGN-	392
Db	233	MFEFFQRTETRTNYPNIFRISNLVMIYIIHWNACVYYSISKAIGFGADTWYYPNTSHP	292
Qy	393	-----EYLCRYWAVRTLITIGLPEPQTLPEIVFOLLNFFSGVFVFSLLIGOMEDVI	445
Db	293	EFARLTRKYVSLYWSLTTLTIGETPPVRDSEYFFVVDLFGVLIFATIVGNVGSMI	352
Qy	446	GAATANQNYFRACMDDTIAYNNYSIPKLQKRVRTWYETWDSQRMDESLLKTLPTT	505
Db	353	SNMNAARAEQAKIDAIKQYMHFNVSKDMEKRVIKWFDYLTWTKKAVDEREVLKPLDK	412
Qy	506	VQLALADVNFPSIISKVDLFGCDTQMIYDMLRLKSVLYLPDGFVCKGKEIGHKMYIHK	565
Db	413	LRAEIAINVHLETLTKKRVIFADCEAGLLVELVLKLPQVYSPGDYICRKGDIGREMYIHK	472
Qy	566	HGEVQVLGGPDGTVLTLKAGSVGEISLLAAGG--GNRRTANVAHGFANLLTLDKK	622
Db	473	EGLAVV-ADGVTVQFVVLSDGSYFGEISILNIGKSGNRTANIRISIGYSDLFCLSKD	531
Qy	623	TLQEILVHYPDSEIRILMKAR-VLLKQKAKTAEATPPRKDLALLPFPKPEETPKFKTLLG	681
Db	532	DLMEALTEYDPAKAMLEKKGQILMKDGLLDIEVANLGSD-----PKOLEEKV--AYME	583
Qy	682	GTG---KASLARLLKLKREQAQKK	703
Db	584	GMDRLQTKFARL--LAEYDAAQKK	606

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 21, 2005, 19:50:39 ; Search time 48 Seconds
(without alignments)
1393.430 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSAEGEEVLTIETVEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3166.5	74.8	610	2	US-09-949-016-6945 Sequence 6945, Ap
2	2202	52.0	416	2	US-09-949-016-11669 Sequence 11669, A
3	1949	46.0	909	2	US-09-538-092-1315 Sequence 1315, Ap
4	857	20.2	698	2	US-09-949-016-10215 Sequence 10215, A
5	850	20.1	694	2	US-09-538-092-1351 Sequence 1351, Ap
6	818.5	19.3	690	2	US-09-275-252A-19 Sequence 19, Appl
7	817	19.3	686	2	US-09-538-092-1037 Sequence 1037, Ap
8	817	19.3	694	2	US-09-949-016-11549 Sequence 11549, A
9	655	15.5	575	2	US-09-927-267-1 Sequence 1, Appl
10	640	15.1	575	2	US-09-927-267-16 Sequence 16, Appl
11	484	11.4	261	2	US-09-275-252A-18 Sequence 18, Appl
12	416.5	9.8	256	2	US-09-270-767-46624 Sequence 46624, A
13	413	9.8	1203	2	US-09-949-016-6615 Sequence 6615, Ap
14	412.5	9.7	910	2	US-08-997-685A-2 Sequence 2, Appl
15	412.5	9.7	910	2	US-08-986-436-31 Sequence 31, Appl
16	412.5	9.7	1109	2	US-09-949-016-10771 Sequence 10771, A
17	405.5	9.6	889	2	US-09-949-016-6036 Sequence 6036, Ap
18	399.5	9.4	855	2	US-09-949-016-7263 Sequence 7263, Ap
19	382.5	9.0	749	2	US-08-997-685A-10 Sequence 10, Appl
20	382.5	9.0	749	2	US-08-986-436-39 Sequence 39, Appl
21	382	9.0	528	2	US-08-997-685A-4 Sequence 4, Appl
22	377.5	8.9	504	2	US-08-086-436-33 Sequence 33, Appl
23	370	8.7	597	2	US-08-997-685A-12 Sequence 12, Appl
24	368	8.7	506	2	US-08-997-685A-6 Sequence 6, Appl
25	368	8.7	506	2	US-08-086-436-35 Sequence 35, Appl
26	368	8.7	597	2	US-08-086-436-41 Sequence 41, Appl
27	360.5	8.5	960	2	US-09-694-777A-21 Sequence 21, Appl

28	349	8.2	987	2	US-09-694-777A-22 Sequence 22, Appl
29	347.5	8.2	962	2	US-09-694-777A-24 Sequence 24, Appl
30	345.5	8.2	962	2	US-09-614-480-9 Sequence 9, Appl
31	345.5	8.2	962	2	US-09-694-777A-3 Sequence 3, Appl
32	345.5	8.2	962	2	US-10-422-075-9 Sequence 9, Appl
33	344	8.1	170	2	US-09-358-383C-27 Sequence 27, Appl
34	337	8.0	988	2	US-10-162-012-12 Sequence 12, Appl
35	336	7.9	989	2	US-09-694-777A-23 Sequence 23, Appl
36	335	7.9	988	2	US-09-614-480-2 Sequence 2, Appl
37	335	7.9	988	2	US-10-162-012-5 Sequence 5, Appl
38	335	7.9	988	2	US-10-422-075-2 Sequence 2, Appl
39	334	7.9	319	2	US-09-358-383C-22 Sequence 4, Appl
40	334	7.9	989	2	US-09-694-777A-4 Sequence 4, Appl
41	317.5	7.5	1159	1	US-08-956-242-13 Sequence 13, Appl
42	317.5	7.5	1159	2	US-09-351-215-13 Sequence 13, Appl
43	317.5	7.5	1159	2	US-09-226-012-2 Sequence 2, Appl
44	317.5	7.5	1159	2	US-09-226-012-4 Sequence 4, Appl
45	317.5	7.5	1159	2	US-09-358-383C-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-6945
; Sequence 6945, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6945
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6945

Query Match	74.8%	Score	3166.5	DB 2	Length	610			
Best Local Similarity	99.0%	Pred. No.	4e-272						
Matches	609	Conservative	0	Mismatches	1	Indels	5	Gaps	1
QY	195	MPLTEYLKRIKLPNSIDSYTDRLVLLMLLVLTAYNNWNCMFIPURLVFPYOTADNIHYWL	254						
DB	1	MPLTEYLKRIKLPNSIDSYTDRLVLLMLLVLTAYNNWNCMFIPURLVFPYOTADNIHYWL	60						
QY	255	IADIICDIYLYDMLFTQPRLOQVRGGDIIVDSNELRKHYRTSTKFDQDVASIIIPFDICY	314						
DB	61	IADIICDIYLYDMLFTQPRLOQVRGGDIIVDSNELRKHYRTSTKFDQDVASIIIPFDICY	120						
QY	315	LFFGFNPMFRANRMLKYTSPEFNHLESIMDKAYIRVIRTTGYLLFILHINACVYWA	374						
DB	121	LFFGFNPMFRANRMLKYTSPEFNHLESIMDKAYIRVIRTTGYLLFILHINACVYWA	180						
QY	375	SNYEGIGTTTWWYDGEYELRCYVAVRLLITIGGLPEPQTLFEIVFOLLNFFSGVVFV	434						
DB	181	SNYEGIGTTTWWYDGEYELRCYVAVRLLITIGGLPEPQTLFEIVFOLLNFFSGVVFV	240						
QY	435	SSLIGQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMLD	494						
DB	241	SSLIGQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKLQKRVRTWYETWDSQRMLD	300						
QY	495	ESDLLKLTPTTVQLALADIVNFISIISKVDLFGKCDTQMIYDMLRLKLSVLYLPGDFVCKK	554						

Db	301	ESDLKLTPTTVQLALADVNFSSISKVDLFGKCDTQMIYDMLLRKSLVLYLFGDVFCKK	360
Qy	555	GEIGKEMYIIKHGEVQVLGGPDGTVLVTLKAGSVFGEISLLAAGGGRNRTANWVAHGFA	614
Db	361	GEIGKEMYIIKHGEVQVLGGPDGTVLVTLKAGSV-----LLAAGGGRNRTANWVAHGFA	415
Qy	615	NLLTLDKKTQLOEILVHYDPDSERILMKKARVLLKQAKTAEATPPRKDLALLPPPKEETPK	674
Db	416	NLLTLDKKTQLOEILVHYDPDSERILMKKARVLLKQAKTAEATPPRKDLALLPPPKEETPK	475
Qy	675	LFKTLGGTGKASLARLLKLKEQAAQKENSEGEGEEKENEDQKENEDKG	734
Db	476	LFKTLGGTGKASLARLLKLKEQAAQKENSEGEGEEKENEDQKENEDKG	535
Qy	735	KENEDKDKGREPEEKPLDORPECTASPIAVEEBPHSVRRVTLPRGTSRQSLIIISMAPSABG	794
Db	536	KENEDKDKGREPEEKPLDORPECTASPIAVEEBPHSVRRVTLPRGTSRQSLIIISMAPSABG	595
Qy	795	GEEVLTIEVKEKAKQ	809
Db	596	GEEVLTIEVKEKAKQ	610

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RESULT 2
US-09-949-016-11669
; Sequence 11669, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11669
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11669

```

Query Match	52.0%;	Score 2202;	DB 2;	Length 416;
Best Local Similarity	99.8%;	Prod. No. 9.2e-187;		
Matches 412;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	114	PQNKPPAAPVINEVADAOQLHNLVKRMQRORTALYKKKLVEGDLSSPEASQPTAKPTAVPPV	173	
Db	1	PQNKPPAAPVINEVADAOQLHNLVKRMQRORTALYKKKLVEGDLSSPEASQPTAKPTAVPPV	60	
Qy	174	KESDDKPTHEHYRLLWPFVKKKWPLTEYLKRIKLNSIDSYTDRLYLLWLLVLTLAYNWC	233	
Db	61	KESDDKPTHEHYRLLWPFVKKKWPLTEYLKRIKLNSIDSYTDRLYLLWLLVLTLAYNWC	120	
Qy	234	WFIPLRLVFPYQTADNHIYMLIADIICDIIYLYDMLFIQPLRQFVRGDDIIVDSNELRKH	293	
Db	121	WFIPLRLVFPYQTADNHIYMLIADIICDIIYLYDMLFIQPLRQFVRGDDIIVDSNELRKH	180	
Qy	294	YRTSTKQLDVASIIPDICYLTFGFNPMPFRANRLKYTSFFEFNHLESIMDKAYIRV	353	
Db	181	YRTSPKQLDVASIIPDICYLTFGFNPMPFRANRLKYTSFFEFNHLESIMDKAYIRV	240	
Qy	354	IRTTGYLLFILHINACVYVWASNYEGITTTWVDGEGNEYLRCYVWVRTLIITIGGLPE	413	
Db	241	IRTTGYLLFILHINACVYVWASNYEGITTTWVDGEGNEYLRCYVWVRTLIITIGGLPE	300	

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Qy 414 PQTLEFVIFQLLNFFSGVVFESSLIQMRDVGIGAAATANQNNTFRACMDDTIAYMNNYSIPK 473
Db 301 PQTLEFVIFQLLNFFSGVVFESSLIQMRDVGIGAAATANQNNTFRACMDDTIAYMNNYSIPK 360
Qy 474 LVQKRVRTWXYEYTWDSORMLDESLLKTLPTTVQLALAIADNVNFSIIISKVDLFPK 526
Db 361 LVQKRVRTWXYEYTWDSORMLDESLLKTLPTTVQLALAIADNVNFSIIISKVDLFPK 413

RESULT 3
US-09-538-092-1315
; Sequence 1315, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538.092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuraPatSeqFormatter Version 0.9
; SEQ ID NO 1315
; LENGTH: 909
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q14028
US-09-538-092-1315

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Query Match	46.0%;	Score 1949;	DB 2:	Length 909;
Best Local Similarity	46.2%;	Pred. No. 9e-164;		
Matches	403;	Conservative 122;	Mismatches 238;	Indels 110;
Gaps	18			
Qy	14	IGENNENPQSSRRNEEGSHFSNOSQOITTAOB--ENKGE--EKS LKTKSTPVTSEEPHTN	68	
Db	67	VGEBAKKEABEAKBEAEVAAEEAEKEPDQWAEETKEPEAEAEAAASSGVFATKOHPEVO	126	
Qy	69	IQDK-----LSKKNSSGDLTTPNDPONAAPTGTVPQEKMDPGKEGPN-----	112	
Db	127	VEDTIDADSCPLMAEENPPS--TVLPSPSPAKSDTLIVPSSASGTHRKKLPDEDDAEELK	184	
Qy	113	--SPQNK-----PAAP-----VINEYADAQLHNLVKRMQRORTALY	146	
Db	185	ALSPAESPVVAWSDPTTPKDTGDQDRAASTASTNSAIND---RLQELVLKFKERTEKV	240	
Qy	147	KKKLVEGDL-----SPASQATKPTAVPPVKESDDKPT--EHYRLLLVFKVKMKPLTEY	200	
Db	241	KEKLIDPDVTSDEESPSPAKKAPAPOTKPAEAPVEEHCYCDMLCKFKHPRWKY	300	
Qy	201	LKRITLNSIDSYTDRLYLWLLLVLTLYANNWCWFILRLRVFPYQADNIHYHLIADIIC	260	
Db	301	----QFQSDLP LTNLMYLWLFVVMANNWCWLIIPVRWAPPYQTPONIIHMLIMDYLC	356	
Qy	261	DIILYDMLFIQRLQFVRGDIIVDSNEURLKHVYRTSTKFQLDVASIIPFDICYLFFGFN	320	
Db	357	DLIYFLDITVFQRLQFVRGDIITDKKDMNNVYLKSRRFKMDLLSLPLDPLFLYLVGVN	416	
Qy	321	PMFRANMLKYTSPFENHHLESIMDKAYIYRVIRTTGYLLFLIHLINACVYYWASNYEGI	380	
Db	417	PLLRPLPCLXYMAFFENSRLESILSKAYVYRVIRTTAYLLYSHLNLSCLYWASAYOQL	476	
Qy	381	GTTIRWYVDGSENYLRCCYNAWRTLITIGLPEPQTLFEIVFOLLNPSGVFVSSLLCO	440	
Db	477	GSTHWYVDGVGNSYIRCCYFAVKTLITIGLPDPKTLFEIVFOLLNYTFVFAFSVMTGO	536	
Qy	441	MRDVIGAATANQYFRACMDDTIAYMNNYSIPKLIVQKRVRTWYETWDSORMLDESLLIK	500	

Db 537 MRDVGAATAGQTYRSCMDSTVKYKMFYKPKSVQNRVKTVEYTWHSQGLDSELMV 596
QY 501 TLPTTQALALADVNFSIIISKVDLFGKCDTQMIYDMLRLKSVLYLPDGFVCKKGIGKE 560
Db 597 QLPDKWRLDALDVNYNIVSKVALFGCDRQMFDMLEKRLSVVLYLPNDYVCKKGIGRE 656
QY 561 MYIIKHGVBQVGGPGDGTQVLTAKGVSFGFISLLAAGGNNRTANVVAHGFANLLTLD 620
Db 657 MYIIQAGQVQVGGPGDGSVLTAKGVSFGFISLLAAGGNNRTANVVAHGFANLLTLD 716
QY 621 KKTQILVHYPPSERILMKARVLKOKATAEATPPKOLALLFPKKEETPKLFTLL 680
Db 717 KCOLNEILVHYPSOKLLRKARMLRSNNK-----PKBEKSVLLIPLPRAGTPKLPNAAL 771
QY 681 GGTGKAS-----LARLLKREOAQKENSCEGEBEGKENEKOKENEDKOK 728
Db 772 AMTGKMGKAGKGLAHLARLKLALALEAAKHEEL---VEQAKSSQDVKEGESAAP 828
QY 729 ENEDKQKE-NEDKDKGREPEEKPLDRPECTASPIAV-----BEPHVSVRTVLP 776
Db 829 DQHTPKAATDPPAPRTPEPE-GSPSPSPASLGSCEGEBEGAEPEEHSVR-----882
QY 777 RGTSRSLIISMAPSAGGSEVLTIEVKEKAKQ 809
Db 883 -----ICMSPGPEGEOILSVKMPERE 906

RESULT 4

US-09-949-016-10215
; Sequence 10215, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-09-08
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10215
; TYPE: PR1
; ORGANISM: Human
US-09-949-016-10215

Query Match 20.2%; Score 857; DB 2; Length 698;
Best Local Similarity 29.9%; Pred. No. 5.2e-67;
Matches 226; Conservative 153; Mismatches 272; Indels 106; Gaps 22;

QY 19 ENEQSRNRGSHPSNQSQTQAQENKGEKSLTKSTPTVTEEPHTNIQDKLSKNS 78
Db 1 QTEKXAKINTQYSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHS 41
QY 79 SGDLTTPDPQNAAEPTGTVEQKMDPGKGNPSPQKPPAAPVINEYADAQLNLVKR 138
Db 42 SSBETS-----SVLPQ-GIAMEIRGLADSGGSGTGO-----GIARSLRIFL 83
QY 139 MRQTALYKKLVGDLSSP-----EASPTAKTAPVPPKESDDKTEHYHLLW 189
Db 84 LRRWAARHVHQDQGPSFDPFRGASLKEYSSQESNAQNVGQBPADRG-----BSAW 138
QY 190 FKVKMPL-----TEYLKIKLPNSI-DSYTORLYLLVLLVTLAYNNWCWFIPL 238
Db 139 -----PLAKCNTWTSNNTEBEKTKKDAIVDPDPSNLYRWLTALPVFYNNWYLLIC 192

QY 239 RLVPYQYADNTHYVLIADIICDIYLYDMLFIQPRLOFVRGCDIIVDSNELRKHYRTST 298
Db 193 RACFDELOSEYUMLWLVLDYSADVLYVLDVL-VRARTGFLBOCLMWSDTNRNLWOHYKTTT 251
QY 299 KFOQDVASIIIPEDICVLPFGFN-PMFRANRMLKYTSFFEFNHHLESIMDKAYIVRVITTT 357
Db 252 QFKLDVLSVPTDLAYLVKVTNYPEVRNRLKLSRLPEFFDRTETRTNYPMFRIGNLV 311
QY 358 GYLLFILHINACYWASVEGIGTRVYDG-----EGNEYLRCYVWAVRTLTITG 409
Db 312 LVILIIHWNACIYFAISKFIGFGTDSWVYPNISIPHEGRLSRKYIYSLYWSLTLLTTIG 371
QY 410 GLPERQTLFEIVFOLLNPFSGVVFSSLTIGDRDVI GAATANQNYFRACMDDTIAYMNY 469
Db 372 ETTPPPVKDEYLVVVDFLVGVLI FATIVGVNWSISNNASRAEFOAKIDSIKQYQFR 431
QY 470 SIPKLQKRVRTWYEYTWDSORMLDESLLKLTPTTVOALALADVNFSIISKVDLFGKD 529
Db 432 KYTKOLETRVIRWFDYLMANKKTVDKEVLKSLPDKLKAELAINVHLDTLKKVRI FODCE 491
QY 530 TQMYDMLRLKSVLYLPDGFVCKKGIGKEKEMVYIIKHGEVOVLGGPDGTVLTKAGSV 589
Db 492 AGLLVELVLKLRPTVPSPGDYICKGDIKEMVYIINEGKLAVV-ADGGVTOFVVLSDGSY 550
QY 590 FGEISLLAAGG---GNRTANVVAHCFANLLTLDKKTLOEILVHYPDSEIRILMKKAR-VL 645
Db 551 FGEISILNTKSGSGNNRTANIRSIGSDLCFCLSKDDLMEALTEYPEAKKALEEGROIL 610
QY 646 LKQK---AKTATPPRKDLALLFPKKEETPKLFTLLGGTGKASLARLL-----KL 694
Db 611 MKDNLIDEELARAGADPKDL-----EKVEQLGSSL--DTLOTRFARULLAEYNATOMKM 662
QY 695 KREQAQKXENEGEGEE---EGKENEKOKENEDKOK 728
Db 663 KQRLSLESQVKGSGDKPLADGGEVPGDATK-TEDKOO 698

RESULT 5

US-09-538-092-1351
; Sequence 1351, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR FILING DATE: 2000-03-29
; PRIOR FILING DATE: 1999-04-01
; PRIOR FILING DATE: 2000-02-01
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapSeqFormatter Version 0.9
; SEQ ID NO 1351
; LENGTH: 694
; TYPE: PR1
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q16281
US-09-538-092-1351

Query Match 20.1%; Score 850; DB 2; Length 694;

Best Local Similarity 30.0%; Pred. No. 2.2e-66;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPSNQSQTQAQENKGEKSLTKSTPTVTEEPHTNIQDKLSKNSGDLTTP 86
Db 5 NTQVSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHSSEETS-- 43
QY 87 DPQNAEPTGTVEQKMDPGKGNPSPQKPPAAPVINEYADAQLNLVKRQRTALY 146

Db 44 ---SVLQP-GIAMETRGADSGQGSFTGQ-----GIARLSRLIFLLRWAARH 87
Qy 147 KKKLVGDLSSP-----EASPTAKPTAVPPVKESDDKPTFHYVYLLAFKVKMPL 197
Db 88 VHQDQGPSFDFRFGAELKEVSSQESNAQNVGQEPADRG-----RSAM-----PL 136
Qy 198 -----TEYLKRIKLPSNI-DSYTRDLXLLMLLVTLAYNMNCFPIRLVPPYQT 246
Db 137 AKCNTWTSNNTTEEEKTKKDAIVDPSSNLYYRMLTAIPALPVYNNYLLICRACFDELQ 196
Qy 247 ANIHVWLADIICDIYLYDMFLFQPRLOFVRGGDIIIVDSNELKHYTSTKFKQDLVAS 306
Db 197 SEYLMVLVDYSADVLYDLVL-VRAITGFLQGLMVDNTRLMOHYKTTTQFKLDVLS 255
Qy 307 IIPFDICYLFFGFN-PMFRANRMLKYTSFPEFNHLESIMDKAYIVRVIRTTGYLLFILH 365
Db 256 LVPTDLAYLVGTYNEVEVFNRLKFSRFEFPDRTETRTNYPMFRIGNLYIILIIH 315
Qy 366 INACVYVWASNYEGIGTTRWVYDG-----EGNEYLRCYVWAVRVLITIGGLPEPOTL 417
Db 316 WNAIVFAISKPIGFGTDSWVYPNISIPEHGRLSRKVIYVSLYWSLTLTLTIGETPPVKD 375
Qy 418 FEIVFOLLNPFSGVVFSSLIQMRDVIGAATANQNYFRACMDDTTAYMNVISIPKLQK 477
Db 376 EYLFVVDVFLVGLVIFATIVGVGSMISNMNASRAEFOAKIDSIRQYMQFRKVTKDLET 435
Qy 478 RVRTVEYTWDSQRMLEDLLKTLPTTVQALAIIDVNFSTIISKVDLFGKCDTQMIYDML 537
Db 436 RVIRFDYLVANKTVDEKEVLKSLDPDKAEIAINVHLDTLKKRIFQDCEAGLLVELV 495
Qy 538 LRLKSVLYLPGDFVCKKGBIGKEMYIIKHGEVOVLGGPDGTVKLVTLKAGSVFGEISLLA 597
Db 496 LKLRPTVSPGDYICKKGDIGREMYIINEGKLAVV-ADGVTQFVVLSDGSYFGEISILN 554
Qy 598 AGG---GNRRTANVAHGFANLLTLDDKTLQELVHYPSERILMKAR-VLLKQK---A 650
Db 555 IRGKSGNRTANIRSIGSDFLFCLSKDDLMALTEYPAKKALEBKGRQILMKNDLIDE 614
Qy 651 KTAETAPPRKDLALLPPKKEETPKLFTLLGGTGKASLARLL-----KLKREQAOK 702
Db 615 ELARAGADPKDL-----BEKVEQLGSLI--DTLQTRFARLLAEYNATQMKQRLSQLE 666
Qy 703 KENSEGEE---EGKENEDKQENEDKQK 728
Db 667 SQVKGCGDKPLADGEVPGDATK-TEDKQK 694

RESULT 6

US-09-275-252A-19
; Sequence 19, Application US/09275252A
; Patent No. 6641997
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/09/275,252A
; CURRENT FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-275-252A-19

Query Match 19.3%; Score 818.5; DB 2; Length 690;
Best Local Similarity 30.0%; Pred. No. 1.3e-63;
Matches 221; Conservative 128; Mismatches 262; Indels 125; Gaps 22;
Qy 5 LTKVAKVPIGNNENQSSRRNEEGSHPS-----NOSQOQTAAEENKKEE-----KSL 53
Db 17 VTMNPVIVP-----DIEKEIRRMENGACSSPESDDSDSAVTSSESENPHARGSFYSKSL 71
Qy 54 KTKSTPVTSEEPHTNIQDKLSKNSGDLTTPNDPQNAEPTGTVPQEKEMDPGKEGPN 113
Db 72 R-KGGSQREQLPGAIATFNVNNS-----NKD-----QEPEEKKKKKKKSKDDKNE 121
Qy 114 PQNKPPAAPVINEYADAOQLHNLKRMORTALYKKKLVGDLSSPEASPTAKTAVPPV 173
Db 122 NKNDPE-----KKKKKKKKKK-----E 141
Qy 174 KESDDKPTHEYVRLWFKVKMPLTEYLKRIKLPSIDSYTRDLXLLMLLVL AYNW 231
Db 142 EKSQDKKEHH-----KKEVVV-----IDP-SCNTYNNMLFCITLPMYNNW 140
Qy 232 NCFPIPLRLVPYOTADNIHYWLIADIICDIYLYDMFLFQPRLOFVRGCDIIVISNELK 291
Db 181 T--MVIARACFDELOSDYLEYWLILDYVSDIVYLIDM FVRTRTGYLEQGLLVKEELKI 237
Qy 292 KHYRTSTKFDLVASIIIPDICYLFFGFN-PMFRANRMLKYTSFPEFNHLESIMDKAYI 350
Db 238 NKYKSNLOPKLDVLSIIPDTLLYFKLGWNPDIRLNRLLRFSRMPFEFFORTETRTNYPNI 297
Qy 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWVY-----DGE---GNEYLRCYVWAV 402
Db 298 PRISNLVMYVIIHWNACVFYSISKALCFGNDTWVYPDINDPEFGLRLARKVYVSLYWS 457
Qy 403 RLITIGGLPEPOTLFEIVFOLLNPFSGVVFSSLIQMRDVIGAATANQNYFRACMDDT 467
Db 358 LTLTTIGETPPVRDSEYFVVVDLGLVLFATIVGNIGSMISNMNARAEFOARIDAI 417
Qy 463 IAYMNYISIPKLQKRVTRTVEYTWDSQRMLEDLLKTLPTTVQALAIIDVNFSTISKV 522
Db 418 KQYMFPRVSKDMKRVIKWFDYLTWNKKTVEKEVYLPDKLRAEIAINVHLOTLLKV 477
Qy 523 DLFGKCDTQMIYDMLRLKLSVLYLPGDFVCKKGBIGKEMYIIKHGEVOVLGGPDGTVKLV 582
Db 478 RIFADCEAGLLVELVLQPVYSPGDYICKKGDIGREMYIIEGKLAVV-ADGVTQFV 536
Qy 583 TLKAGSVFGEISLLAAGG---GNRRTANVAHGFANLLTLDDKTLQELVHYPSERILM 619
Db 537 VLSDGSTFGEISILNIRKSGNRETANIKSIGSDLFCLSKDDLMALTEYPAKTMLE 596
Qy 640 KXARVLLKQK----KTAETAPPRKDLALLPPKKEETPKLFTLLGGTGKASLARLL--- 692
Db 597 EKGQILMKDGLLDLNIANAGSDPKDLEEKVTRMEGSDVLLQT-----RPARILADY 648
Qy 693 -----KLKREQAOKK 703
Db 649 ESMQKQLKQLRTKVEK 664

RESULT 7

US-09-538-092-1037
; Sequence 1037, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965

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; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqformatter Version 0.9
; SEQ ID NO 1037
; LENGTH: 686
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P29973
US-09-538-092-1037

Query Match
Best Local Similarity 19.3%; Score 817; DB 2; Length 686;
Matches 226; Conservative 129; Mismatches 266; Indels 136; Gaps 24;

QY 5 LTKVNVKPIGENNENQSSRRNEEGSHPS-----NOSQOTTAQENKGE-----KSL 53
DB 13 VTMPNVIVP-----DIEKEIRRMENGACSSFSDDDSASTSESENENPHARGSFYSKSL 67
QY 54 KTKSTPTVTEEPHTNIQDKLSKNSGDLTTPDPQNAAEPTGTVPEQKEMDPEGKGPS 113
DB 68 R-KGGSQREQLPGAIALFNVNSS-----NKD-----QEPBEKKKKKKSKSDKNE 117
QY 114 POKKPPAAPVINEYADAQLHNLVKRMORTALYKKLVGDLSSPEASPTAKPTAVPPV 173
DB 118 NKNDPE-----KXKKKKKKKK-----E 137
QY 174 KESDDKPTHEYRLMFKYKMKPLTEYLKRIKLPNSIDSYDRLYLWLLLVLT--AYNW 231
DB 138 EKSDDKKEE-----KKEVV-----IDP--SGNTYYNWLFCITLPVMYNW 176
QY 232 NCWFILPLRVFPYQADNIHYMLIADIICDIIVLYDMLFIQPLQFVGGDIIVDSNELR 291
DB 177 T--MVIARACFDELQSDYLEWILDYVSDIVYLIDM--FVRTGTGYLEOGLLVKEELKI 233
QY 292 KHYRTSTKFOLDVASIIPFDICVLPFGFN--PMFRANRMLKYTSFFPFNHHLESIMDKAYI 350
DB 234 NKYSNLQPKLDVLSLIPTDLYFKLGWNYPEIRLNRLRFRSMFEFFORTETRTNYPNI 293
QY 351 YRVIRTTGYLLFILHINACVYVWASNYEGIGTTRWY-----DGE-----GNEYLCRYWAV 402
DB 294 FRISNLVMYVIIHWNACVFSISKAIGFGNDTWVYPDINDPEFGLRARKYVYSLWST 353
QY 403 RTLITIGLPEPOTLPEIVFOLLNFFSGVVFSSLIQOMRDVIGAATANONYFRACMDOT 462
DB 354 LTLTTIGETPPPPRDSEYVFWVDFLIGVLIFATIVGNISMSINWNAARAEQARIDAI 413
QY 463 IAYMNNYSIPKLQKRVRTWYETWDSQRMLEDSDLLKTLPTTVQLALADIVNFSIISKV 522
DB 414 KQYMHFRNVSKDMKRVIKWFDYLTWTKTVDEKEVLKYLDPDKLRAEIAINVHLDLTKKV 473
QY 523 DLPFGCDTQMIYDMLRLKSVLYLPDGVCKKGEIGKEMYIIKHGEVOVLGGPDGTVLV 582
DB 474 RIFADCEAGLLVELVLKLPQVYSPGDYICKKGDI GREMYIIKEGLAVV--ADDGVTVQV 532
QY 583 TLKAGSVFGISILAAAG---GNRRTANVVAHGFANLLTLDKKTLQBIHVYDSEIRLM 639
DB 533 VLSGYSVFGISILINIKSGKAGNRRTANIKSIGYDLFCISKODLMEALTEYDPAKTMLE 592
QY 640 KQARVLLKQKA-----KTAEATPPRKOLALLFPKKEETPKLFTLLGGTGKASLARLL--- 692
DB 593 EKGQILMKDGLLDLNIANAGSDPKDLEEKVTRMEGSDVLLQT-----RFAIILAEY 644
QY 693 -----KLKREQAOKK-----ENSEG--GEEG 713
DB 645 ESMOQKLQRLTKVKEFKLPLIDTEFSSIEGPGAEG 681

RESULT 8
US-09-949-016-11549
; Sequence 11549, Application US/09949016

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Qy	693	-----KLKEQQAOKK-----ENSEG-GEERG 713
Db	653	ESMQQKQKQLTKVFKLPLDTESSIEGPGAESG 689
RESULT 9		
US-09-927-267-1		
; Sequence 1, Application US/09927267		
; Patent No. 6933147		
; GENERAL INFORMATION:		
; APPLICANT: Creech, Christopher D.		
; APPLICANT: Jegla, Timothy J.		
; APPLICANT: ICAGEN, Inc.		
; TITLE OF INVENTION: Channel		
; FILE REFERENCE: 018512-006510US		
; CURRENT APPLICATION NUMBER: US/09/927,267		
; CURRENT FILING DATE: 2001-08-10		
; PRIOR APPLICATION NUMBER: US 60/226,253		
; PRIOR FILING DATE: 2000-08-17		
; NUMBER OF SEQ ID NOS: 16		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 1		
; LENGTH: 575		
; TYPE: PRT		
; ORGANISM: Homo sapiens		
; FEATURE:		
; OTHER INFORMATION: cyclic nucleotide-gated cation channel 2B (CNG2B)		
US-09-927-267-1		
Query Match 15.5%; Score 655; DB 2; Length 575;		
Best Local Similarity 29.2%; Pred. No. 3.3e-49;		
Matches 165; Conservative 121; Mismatches 241; Indels 38; Gaps 14;		
Qy	202	KRIKLPNSDSTDRILYLLWLLVTLAYNNWCFPLRLVFPYQTADNIHYWLIADIICD 261
Db	19	KARKLPVLDPDSDG-YYYWMLNTVFPVNNLIILVCRACFDQLQHGIVLAWLVLDYTS 77
Qy	262	IIVLYDMLFIQRLQPVRCGDIIVDSNELRKHYRTSTKFQLDVASIIPDFICYLFFGF-EN 320
Db	78	LHLYLDMV-VRHTEGLEGILVVDKGRISRYRTWSFFLDASLMPDVTVDVYVRLGPH 136
Qy	321	PMFRANRMLKYTSFFENHLESIMDKAYIYRVIRTTGYLLFILHINACVYVWASNYEGI 380
Db	137	PTLRNRLFLRAPLPEAFDRTETRTAYPNAFRIAKMLYIFVVIHNSCLYFALSRYLGF 196
Qy	381	GTRWYVDGEG-----NEVLCRYVAVRTLTITIGGLPEPOTLFEIVFOLLNFFSGVP 432
Db	197	GRDAWYPPDPAQGFERLRQYLSYFSFTLITVTGDTPTTAREBEYLFMVGDFLLAYM 256
Qy	433	VFSSILIGMRDVI-GAATANONYFRACMDDTIA--YMNYSIPKLQKRVRTWYETWDS 489
Db	257	GFATIMGSMSSVIYNNMTADAFY----PDHALVKYKMKLQHVNRKLRERRVIDWYQHLQIN 313
Qy	490	QRMLDESLLKLTPTTVQLALADIVNFSIISKVDLFGKCDTOMIYDMLRLKSLVLYLPGD 549
Db	314	KQWTEVAILOQLPERLRAEVAVSVHLSTLSRVQIFQNCESALLEELVLKLPQTSVSGE 373
Qy	550	FVCKKGEIGEKEMVYIKHGEVOVLGGPDGKVLVTLKAGSVFGEISLLAAGG---GNRRTA 606
Db	374	YVCRKGDIGQEMYIIRREGOLAVV-ADGGITQYAVLGAGLYFGEISINIKGNMSGNRRTA 432
Qy	607	NNVAHGFANLLTLDKKTLOEILVHPDSEIRILMKKAR-VLLK-----QAKTA--EA 655
Db	433	NTKSLGYSDLFCLSKEDLREVSLEYFQQTIMEEKGREILLKMNKLDVNAEAAEIALQEA 492
Qy	656	TPPRKDLALLFPFKETPTKLFKTLGGTGKASLARLLKLKREQAOKK----ENSEGSEE 711
Db	493	TESR--LRGLDQQLDQTKFARLLAELESSALKIAYRIERLEWQTRWPMPEADAEADD 550
Qy	712	EKENEDKQKEDKQKEDKQKE 736
; Sequence 18, Application US/09275252A		
; Patent No. 6641997		
RESULT 11		
US-09-275-252A-18		
; Sequence 18, Application US/09275252A		
; Patent No. 6641997		
Db	551	EGEPEEGTSKDDEGRASQEGPPGPE 575
RESULT 10		
US-09-927-267-16		
; Sequence 16, Application US/09927267		
; Patent No. 6933147		
; GENERAL INFORMATION:		
; APPLICANT: Creech, Christopher D.		
; APPLICANT: Jegla, Timothy J.		
; APPLICANT: ICAGEN, Inc.		
; TITLE OF INVENTION: Channel		
; FILE REFERENCE: 018512-006510US		
; CURRENT APPLICATION NUMBER: US/09/927,267		
; CURRENT FILING DATE: 2001-08-10		
; PRIOR APPLICATION NUMBER: US 60/226,253		
; PRIOR FILING DATE: 2000-08-17		
; NUMBER OF SEQ ID NOS: 16		
; SOFTWARE: PatentIn Ver. 2.1		
; SEQ ID NO 16		
; LENGTH: 575		
; TYPE: PRT		
; ORGANISM: Rattus norvegicus		
; FEATURE:		
; OTHER INFORMATION: rat cyclic nucleotide gated cation channel 1XNC2		
US-09-927-267-16		
Query Match 15.1%; Score 640; DB 2; Length 575;		
Best Local Similarity 29.1%; Pred. No. 7.1e-48;		
Matches 157; Conservative 114; Mismatches 224; Indels 44; Gaps 14;		
Qy	218	YLLWLLLVTLAYNNWCFPLRLVFPYQTADNIHYWLIADIICOIILYLYDMLFIQPLQF 277
Db	34	YWWMLNTVFPVNNLIILVCRACFDQLQHSYLVAVFVLDYTSLLYLLD-IGVRFHTGF 97
Qy	278	VRGSDIIVDSNELRKHYRTSTKFQLDVASIIPDFICYLFFGFN-PMFRANRMLKYTSFFE 336
Db	93	LEOGILVVDKGMIAISRYRTWSFFLDLASLVPTDAAYVOLGPHIPTLRNRLFRVPLRFE 157
Qy	337	FNHLESIMDKAYIYRVIRTTGYLLFILHINACVYVWASNYEGICTTRWYVDGEG- 491
Db	153	APDRTETRTAYPNAFRIAKMLYIFVVIHNSCLYFALSRYLFGFGRDAWYVDPDPAQGPE 212
Qy	392	---NEVLCRYVAVRTLTITIGGLPEPOTLFEIVFOLLNFFSGVFVFSLLIGQMRDVI 447
Db	213	RLRRQYLSYFSFTLITVTGDTPLPDREBEYLFMVGDFLLAVMGFATIMGSMSSVIYNNM 272
Qy	448	ATANONYFRACMDDTIA--YMNYSIPKLQKRVRTWYETWDSQRMLEDSDLLKLTPTT 505
Db	273	NTADAAFY---PDHALVKYKMKLQHVNRKLRERRVIDWYQHLQINKKMTNEVALQHLPER 129
Qy	506	VQLALADIVNFSIISKVDLFGKCDTOMIYDMLRLKSLVLYLPGDFVCKKGEIGKEMVYIK 565
Db	330	LRAEVAVSVHLSTLSRVQIFQNCESALLEELVLKLPQTSVSGEYVCRKGDIGREMYIIR 389
Qy	566	HGEVOVLGGPDGKVLVTLKAGSVFGEISLLAAGG---GNRRTANVVAHGFANLLTLDKK 622
Db	390	EQGLAVV-ADGGITQYAVLGAGLYFGEISINIKGNMSGNRRTANIKSLGYSDLFCLSK 448
Qy	623	TLQELIVHYPDSEIRILMKKAR-VLLK-----QAKTA--EATPPRKDLALLFPFKEE 671
Db	449	DLREVLSEYVQAQVMEEEKGREILLKMNKLDVNAEAAEIALQEAESR LKGLDQQLDQ 506
Qy	672	TPKLFKTLGGTGKASLARLLKLKX -----EQAAQKKENSEGEEGKENEUK 711
Db	507	LQTKFARLLAELESSALKIAYRIERLEWQTRWPMPEADAEPEGGTSKDEGK 565
; Sequence 18, Application US/09275252A		
; Patent No. 6641997		

QY 432 FVSSLIQMRDVIGATANQNYFRACMDDTTAYMNNYSIPKLVQKRVTVWYETWDSOR 491
DB 504 TCYAMPFIGHATALLQSLDSSRRQYQKQVEQYMSFHKLPDPTRQRIHDYEHRYQG-K 562
QY 492 MDESLLKTLPTTQALALADNFS---IISKVDLFGKCDTQMIYDMLLRLKSLVLYLPG 548
DB 563 MDESILGELSEPLREEI---INFNCRKLVASMLFANADPNFVMSLTKURFEVFPQ 619
QY 549 DFVCKKGEIGKEMYIIKHGEVOVL-GGPDGTQKLVTLKAGSVFGEISLLAAGGNNRRRTAN 607
DB 620 DVIIRREGTIKKMYFIQHGVSVLTKGNKTK---LADGSYFGEICLLTRG---RRTAS 672
QY 608 VVAHGFANLLTDKKTQLBILVHYDPDSERILMKKA 642
DB 673 VRADTYCRLYSLSDVNFNEVLBEYP-----MMRRA 702

RESULT 14

US-08-997-685A-2
; Sequence 2, Application US/08997685A
; Patent No. 6551821
; GENERAL INFORMATION:
; APPLICANT: The Trustees of Columbia University
; APPLICANT: Kandel, Eric
; TITLE OF INVENTION: Brain Cyclic Nucleotide Gated Ion Channel and Uses Thereof
; FILE REFERENCE: 0575/54806
; CURRENT APPLICATION NUMBER: US/08/997,685A
; CURRENT FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

LENGTH: 910
TYPE: PRT
ORGANISM: mouse
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (130)..(148)
OTHER INFORMATION: S1
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (164)..(185)
OTHER INFORMATION: S2
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (208)..(229)
OTHER INFORMATION: S3
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (243)..(271)
OTHER INFORMATION: S4
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (291)..(313)
OTHER INFORMATION: S5
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (332)..(358)
OTHER INFORMATION: P
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (367)..(387)
OTHER INFORMATION: S6
FEATURE:
NAME/KEY: DOMAIN
LOCATION: (472)..(602)
OTHER INFORMATION: CNB
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: AAC53518
DATABASE ENTRY DATE: 1997-12-27
RELEVANT RESIDUES: (1)..(910)
US-08-997-685A-2

Query Match

9.7%; Score 412.5; DB 2; Length 910;

Best Local Similarity 20.2%; Pred. No. 2.3e-27;
Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;
QY 210 IDSYTD-RLYLWLLLVLTAYNNWNCWFPLRLVPPYQADNIHYWLIADIICDIIYLVDM 268
DB 124 IHPYSDFRPY--WDLIMIMMVGNLVLIIPVGITP--FTEQTTTPWIFNVASDTVFLDL 179
QY 269 LFIQPLRQVFRG-----GDIIVDSNELRKHYRTSTKFLQDVASIIFFDICVL 415
DB 180 I-----MNFRTGTVNEDSSSEIILDPKVIKMYLKSWM-FVDFISSIPVDYIFLIVEKMD 233
QY 316 -----FFGNPMFRANMLKYTSFPFENHLESIMDKAY-----YRVRTTGY 459
DB 234 SEVYKTARALRIVREFTKILSLRLRLRLRYIHOWEEIFHMTYDVLASAVVRIFNLICM 293
QY 360 LLFILHINACVY-----WASNYEGIGTTRWVYDGEYLCYCYWAVRTLIT 407
DB 294 MLLCHWDGCLQFLVPLLDPPDCWVSLNE-----MVNSWGQYYSALFKAMSHMLC 447
QY 408 IG-GLPEPQTLFEIVFOLLNFFSGVVFSSLIQMRDVIGATANQNYFRACMDDTIAYM 466
DB 348 IGYGAQAPVMSMDLWITWLSMIVGATCYAMFVGHATALIQSLDSSRRQYQKQVEQY 407
QY 467 NNYSPKLVQKRVTVWYETWDSQRMDESLDKTLPTTQALALADNFS---IISKVD 523
DB 408 SPFKLPADMRQKIHDIYEHRYQG-KIFDEENILSELNDPLREEI---VNFNCRKLIVATMP 463
QY 524 LFKGCDTQMIYDMLLRLKSLVLYLPGDFVCKKGEIGKEMYIIKHGEVOVLGGPDGTQKLV 583
DB 464 LFANADPNFVTAMLSKLRFEVFPQGDYIIRGAVGKMYFIQHGVAQVI-----TKSKE 518
QY 584 LKA--GSVFEISLLAAGGNNRRRTANVVAHGFANLLTLDKKTQLBILVHYDPDSER 636
DB 519 MKLTDGSYFGEICLLTKG---RRTASVRADTYCRLYSLSDVNFNEVLBEYPMRRAFEV 575
QY 637 -----ILMKK-----ARULLKOKAK----- 651
DB 576 AIDRLDRIGKKNISILLOKFKDLNTGVFNNOENEILKQIVKHDRMVOAIPPIYNPOMTA 635
QY 652 ---TAEATPRKDL----- 668
DB 636 LNCSTSTTTPTSRMRTQSPVYVATATSLSHSNLHSPSPSTQTPQPSAILSPSYTTAVTAV 695
QY 669 KEETPKLFTLLGGTGKASLARLLKLKREAAQ---KKENSEGEGEGEKENEKUKENED 725
DB 696 PIQSPLATRTTHYASPTASQLSLMQPOQOOLPOSOVOOTOTOTOTOOOOXXXXXX 700
QY 726 KKENEDKGENEDKDKGREPEEKPLDRPECTASPIAVEEPHVSRRVTLPRGTSKQSL 784
DB 756 QQQQQQQQQQQQQQQQQQQQQQPTFGSSTPKNEVHKSTOALHNTLTKVRLPLSASQPSLP 815
QY 785 -----IISMAPSAEGGEEVLT 801
DB 816 HEVSTLIS-RPHPTVGESLASI 836

RESULT 15

US-09-086-436-31
; Sequence 31, Application US/09086436
; Patent No. 6703485
; GENERAL INFORMATION:
; APPLICANT: Kandel, Eric R.
; APPLICANT: Santoro, Bina
; APPLICANT: Bartsch, Dusan
; APPLICANT: Siegelbaum, Steven
; APPLICANT: Tibbs, Gareth
; APPLICANT: Grant, Seth
; TITLE OF INVENTION: Brain or Heart Cyclic Nucleotide Gated Ion Channel and
; FILE REFERENCE: 0575/54806-A
; CURRENT APPLICATION NUMBER: US/09/086,436
; CURRENT FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 67


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 910
; TYPE: PRT
; ORGANISM: Murine
; US-09-086-436-31

Query Match
Best Local Similarity 20.2%; Pred. No. 2.3e-27;
Matches 150; Conservative 144; Mismatches 269; Indels 179; Gaps 25;

QY 210 IDSYTD-RLVLLLVLTAYNWCNWFIPLRVFPYQTDADNIHYWLIADIICDIIYLYDM 268
Db 124 IHPYSDFRY--WDLIMLVNGLVLIIPVGITF--FTEOTTPWIIFNVASDFVLLDL 179
QY 269 LFIQRLQFVRG-----GDIIIVDSNELRKHRTSTKQFQDVASIIIPFDICYL----- 315
Db 180 I-----MNFTGTWNEDSSEIILDPKVIKMYLKS--FVDFISSIPVDYIFLIVEKGM 233
QY 316 -----FFGFNPMFRANMLKYTSPFENHLESIMDKAY-----IYRVIRTTGY 359
Db 234 SEVVKARALRIVRFTKILSLRLRLRLIRIYIHOWEEIFHMTYDLASAVVRIFNLIGM 293
QY 360 LFIILHINACVY-----WASNYEGIGTTRWYVDGEGNEVLCYHWAVRLIT 407
Db 294 MLLCHWDGCLQFLVLPLOPPPCWVSLNE-----MVNDSWGKQYSYALFKAMSHMLC 347
QY 408 IG-GLPEPQTLFEIVFOLLNFFSGVFVFSLLIGQMRDVGAAATANQNYFRACMDDTIAYM 466
Db 348 IGYGAQAPVMSDLWITWLSMIVGATCYAMFVGHATALIOSLSSRRQYQEKYQVEQYM 407
QY 467 NNTSIPKLQKRVRTYETWDSQRLMDESLLKTLPTTVOLALADVNFS-----IISKVD 523
Db 408 SPFKLPADMRQKIDHYEHRYQG-KIPDEENILSELNDPLREBI---VNFNCRKLVATMP 463
QY 524 LFKGCDTQMIYDMLRLKSLVLYLPDGFCKKGIGKEMYIIKHGEVQVLGPDGTVLVT 583
Db 464 LFANADPNFTYAMLKSLRPFVQPGDYIIRREGAVGKMYFIQHGAVGI-----TKSKE 518
QY 584 LKA--GSVFGEISLLAAGGNGRRTANVAVHGFANLLTLDKKTLOEILVHYPDSE----- 636
Db 519 MKLTDGSYFGEICLLTKG---RRTASVRADTYCELISLSDNFEVLEEEYPMRRAPETV 575
QY 637 -----ILMKK-----ARVLLKOKAK----- 651
Db 576 AIDRLDRIGKNSILLQFKQKDLNTGVFNNOENEILKQIVKHDREMVQAIPINYPOMTA 635
QY 652 ---TAEATPPRKDL-----ALLFP-----P 668
Db 636 LNCTSTTTPTSRMRTQSPVYTATSLSHNLHSPSPSTQTPQPSAILSPCSYTTAVCSP 695
QY 669 KEETPKLFTLLGGTGASLARLLKLKQAAQ---KKENSEGGEEGEKEDKQKED 725
Db 696 PIQSPLATRTFHYASPTASQLSMQPPQQQLPQSOVQQTQTQTQOQQOQQOQQOQQO 755
QY 726 KQKEDKQKEDKQKREPEKPLDRPECTASPIAVEEPHSVRRTVLPRTGTSQSL- 784
Db 756 QQQQQQQQQQQQQQQQQQQQQPQTPGSGSTPKNEVHKSTQALHNTLTKVRLPSASQPSLP 815
QY 785 -----IISMAPSAGGGEVLTI 801
Db 816 HEVSTLIS-RPHPTVGSLSASI 836
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Job time : 51 secs

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OM protein - protein search, using sw model

Run on: December 21, 2005, 19:50:54 ; Search time 166 Seconds
(without alignments)
2036.289 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFKSLTKVKNVKPIGENNEN.....PSAEGGEEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4228	99.9	809	3	US-09-855-828-13
3	3217	76.0	615	5	US-10-978-282-14
4	1952	46.1	1245	5	US-10-978-282-12
5	1781.5	42.1	652	5	US-10-450-763-57830
6	1103	26.1	1037	6	US-11-097-143-26427
7	1088	25.7	644	5	US-10-450-763-35825
8	1052.5	24.9	821	5	US-10-978-282-19
9	955	22.6	747	5	US-10-450-763-42328
10	906	21.4	237	4	US-10-189-507-11
11	902	21.3	237	4	US-10-189-507-7
12	850	20.1	694	3	US-09-842-758-75
13	850	20.1	694	3	US-09-855-828-14
14	850	20.1	694	4	US-10-345-680-26
15	850	20.1	694	4	US-10-174-333-75
16	850	20.1	694	5	US-10-978-282-11
17	829	19.6	663	5	US-10-029-677-16
18	829	19.6	663	5	US-10-978-282-17
19	825.5	19.5	664	4	US-10-029-677-24
20	820.5	19.4	664	4	US-10-029-677-2
21	820	19.4	732	3	US-09-842-758-73
22	820	19.4	732	4	US-10-029-677-15
23	820	19.4	732	4	US-10-174-333-73
24	820	19.4	732	5	US-10-978-282-16
25	819.5	19.4	664	3	US-09-735-927-2
26	819.5	19.4	664	4	US-10-034-843-2
27	819.5	19.4	664	4	US-10-168-651-7

28	819.5	19.4	664	4	US-10-114-153-18	Sequence 18, Appl
29	819.5	19.4	664	5	US-10-978-282-10	Sequence 10, Appl
30	818.5	19.3	664	3	US-09-735-927-4	Sequence 4, Appl
31	818.5	19.3	690	5	US-10-978-282-9	Sequence 9, Appl
32	817	19.3	690	3	US-09-855-828-15	Sequence 15, Appl
33	805.5	19.0	664	5	US-10-978-282-18	Sequence 18, Appl
34	804	19.0	664	4	US-10-029-677-18	Sequence 18, Appl
35	804	19.0	664	4	US-10-087-217-2	Sequence 2, Appl
36	804	19.0	664	4	US-10-295-573-8	Sequence 8, Appl
37	804	19.0	664	5	US-10-978-282-2	Sequence 2, Appl
38	802	18.9	664	4	US-10-295-573-5	Sequence 5, Appl
39	795	18.8	664	4	US-10-087-217-4	Sequence 4, Appl
40	795	18.8	664	5	US-10-978-282-4	Sequence 4, Appl
41	791	18.7	664	4	US-10-087-217-6	Sequence 6, Appl
42	791	18.7	664	4	US-10-295-573-6	Sequence 6, Appl
43	791	18.7	664	5	US-10-978-282-6	Sequence 6, Appl
44	782	18.5	664	4	US-10-087-217-8	Sequence 8, Appl
45	782	18.5	664	5	US-10-978-282-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-09-855-828-1
; Sequence 1, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Cretech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-00601005
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human cyclic nucleotide-gated cation channel (CNG)
; OTHER INFORMATION: 3B (CNG3B)
US-09-855-828-1

Query Match	100.0%	Score 4234;	DB 3;	Length 809;
Best Local Similarity	100.0%;	Pred. No. 5.1e-301;		
Matches 809;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MFKSLTKVKNVKPIGENNENEQSSRRNEEGSHPSNSQQTAAQENKGEKSLTKSTPV	60	
Db	1	MFKSLTKVKNVKPIGENNENEQSSRRNEEGSHPSNSQQTAAQENKGEKSLTKSTPV	60	
Qy	61	TSSEPHNTIQQKLSKKNSSGDLTTNPDQNAASPTGTVPEQKMDPGKEGPNQKPPA	120	
Db	61	TSSEPHNTIQQKLSKKNSSGDLTTNPDQNAASPTGTVPEQKMDPGKEGPNQKPPA	120	
Qy	121	APVINEYADQALNLYKRMQRORTALYKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP	180	
Db	121	APVINEYADQALNLYKRMQRORTALYKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP	180	
Qy	181	TEHYRYLLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYLWLLVTLAYNWCWFIPLRL	240	
Db	181	TEHYRYLLWFKVKMPLTEYLKRIKLPNSIDSYTDRLYLWLLVTLAYNWCWFIPLRL	240	
Qy	241	VFPYQTADNTHYWLIIADIIICDIIYLDMLFIQPRLOFVRGCDIIVDSNELRKHYRTSTKF	300	
Db	241	VFPYQTADNTHYWLIIADIIICDIIYLDMLFIQPRLOFVRGCDIIVDSNELRKHYRTSTKF	300	
Qy	301	QLDVASIIIPDICYLFFGFNPMFRANMLKYTSFFEFNHHLESIMDKAYIYRVIRTTCYL	360	

Db	301	QLDVASIIPFDICYLFFGPNMFRANRMLKYSFFEFNHLESIMDKAYIRVIRTTGYL	360	Db	121	APVINEYADAQLHNLVKRMQROTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP	180
Qy	361	LFILHINACVYWASNYEGITTRWYVDGEGNEYLRCYVAVRTLTITIGGLPEPOTLPEI	420	Qy	181	TEHYVRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTDRLVLLMLLVTLAYNNNCWFIPURL	240
Db	361	LFILHINACVYWASNYEGITTRWYVDGEGNEYLRCYVAVRTLTITIGGLPEPOTLPEI	420	Db	181	TEHYVRLWLFVKVKKMPLTEYLKRIKLPNSIDSYTDRLVLLMLLVTLAYNNNCWFIPURL	240
Qy	421	VFQLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKL VQKRV	480	Qy	241	VFPYOTADNIHWLTIADII CDIIYLYDMLFIQPRLOQFVRGGDII VDSNELRKHYRTSKF	300
Db	421	VFQLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKL VQKRV	480	Db	241	VFPYOTADNIHWLTIADII CDIIYLYDMLFIQPRLOQFVRGGDII VDSNELRKHYRTSKF	300
Qy	481	TYEYTWDSQRMDESDLLKTLPTTVQLALADVNFSIISKVDLFGKCDTQMIYDMLRL	540	Qy	301	QLDVASIIPFDICYLFFGPNMFRANRMLKYSFFEFNHLESIMDKAYIRVIRTTGYL	360
Db	481	TYEYTWDSQRMDESDLLKTLPTTVQLALADVNFSIISKVDLFGKCDTQMIYDMLRL	540	Db	301	QLDVASIIPFDICYLFFGPNMFRANRMLKYSFFEFNHLESIMDKAYIRVIRTTGYL	360
Qy	541	KSVLYLPDGFVCKKGEGIKEMWIIKHGEVOVLGGPDGTVLTAKAGSVFGEISLLAAGG	600	Qy	361	LFILHINACVYWASNYEGITTRWYVDGEGNEYLRCYVAVRTLTITIGGLPEPOTLPEI	420
Db	541	KSVLYLPDGFVCKKGEGIKEMWIIKHGEVOVLGGPDGTVLTAKAGSVFGEISLLAAGG	600	Db	361	LFILHINACVYWASNYEGITTRWYVDGEGNEYLRCYVAVRTLTITIGGLPEPOTLPEI	420
Qy	601	GNRRTANVAHGFANLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK	660	Qy	421	VFQLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKL VQKRV	480
Db	601	GNRRTANVAHGFANLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK	660	Db	421	VFQLNFFSGVVFSSLIQMRDVI GAATANQNYFRACMDDTIAYMNNYSIPKL VQKRV	480
Qy	661	DLALLFPKKEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEGEGEKENEDKQ	720	Qy	481	TYEYTWDSQRMDESDLLKTLPTTVQLALADVNFSIISKVDLFGKCDTQMIYDMLRL	540
Db	661	DLALLFPKKEETPKLFTLLGGTGKASLARLLKLKREQAQKENSEGEGEGEKENEDKQ	720	Db	481	TYEYTWDSQRMDESDLLKTLPTTVQLALADVNFSIISKVDLFGKCDTQMIYDMLRL	540
Qy	721	KENEDKQKENEKDKGNEEDKDKGREPEEKPLDRPECTASPIAVEEPHVSVRTVLPGRGTS	780	Qy	541	KSVLYLPDGFVCKKGEGIKEMWIIKHGEVOVLGGPDGTVLTAKAGSVFGEISLLAAGG	600
Db	721	KENEDKQKENEKDKGNEEDKDKGREPEEKPLDRPECTASPIAVEEPHVSVRTVLPGRGTS	780	Db	541	KSVLYLPDGFVCKKGEGIKEMWIIKHGEVOVLGGPDGTVLTAKAGSVFGEISLLAAGG	600
Qy	781	RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809		Qy	601	GNRRTANVAHGFANLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK	660
Db	781	RQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809		Db	601	GNRRTANVAHGFANLLTLDKKTLOEILVHYPDSEIRILMKKARVLLKQAKTAEATPPRK	660
RESULT 2							
US-09-855-828-13							
; Sequence 13, Application US/09855828							
; Publication No. US20040137433A1							
; GENERAL INFORMATION:							
; APPLICANT: Creech, Christopher D.							
; APPLICANT: Jegia, Timothy J.							
; APPLICANT: ICAGEN, Inc.							
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel							
; FILE REFERENCE: 018512-006010US							
; CURRENT APPLICATION NUMBER: US/09/855, 828							
; CURRENT FILING DATE: 2001-05-14							
; PRIOR APPLICATION NUMBER: US 60/204,445							
; PRIOR FILING DATE: 2000-05-15							
; NUMBER OF SEQ ID NOS: 16							
; SOFTWARE: PatentIn Ver. 2.1							
; SEQ ID NO 13							
; LENGTH: 809							
; TYPE: PRT							
; ORGANISM: Homo sapiens							
; FEATURE:							
; OTHER INFORMATION: CNG3B							
US-09-855-828-13							
Query Match 99.9%; Score 4228; DB 3; Length 809;							
Best Local Similarity 99.9%; Pred. No. 1.4e-300;							
Matches 808; Conservative 0; Mismatches 1; Indels 0; Gaps 0;							
Qy	1	MFKSLTKVNVKPIGNNENEGSSRRNEGSHPSNQSQOTTAQENKGEESLTKSTVP	60	Qy	1	MFKSLTKVNVKPIGNNENEGSSRRNEGSHPSNQSQOTTAQENKGEESLTKSTVP	60
Db	1	MFKSLTKVNVKPIGNNENEGSSRRNEGSHPSNQSQOTTAQENKGEESLTKSTVP	60	Db	1	MFKSLTKVNVKPIGNNENEGSSRRNEGSHPSNQSQOTTAQENKGEESLTKSTVP	60
Qy	61	TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEMDPGKGNPSPQNKPPA	120	Qy	61	TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEMDPGKGNPSPQNKPPA	120
Db	61	TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEMDPGKGNPSPQNKPPA	120	Db	61	TSEEPHTNIQDKLSKNSSGDLTTNPDQNAAEPTGTVPQEMDPGKGNPSPQNKPPA	120
Qy	121	APVINEYADAQLHNLVKRMQROTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP	180	Qy	121	APVINEYADAQLHNLVKRMQROTALYKKKLVEGDLSSPEASPTAKPTAVPPVKESDDKP	180

RESULT 3
US-10-978-282-14
; Sequence 14, Application US/10978282
; Publication No. US20050221426A1
; GENERAL INFORMATION:
; APPLICANT: YAO, Yong
; APPLICANT: CAO, Liang
; APPLICANT: LU, Jianming
; APPLICANT: LLORENTE, Isabel
; TITLE OF INVENTION: Novel Cell-Based Assays Employing Voltage and Calcium Dyns
; FILE REFERENCE: 062614-5002-US
; CURRENT APPLICATION NUMBER: US/10/978,282
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: US 60/589,012
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/515,442
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 10/087,217
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/330,663
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 615

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(615)
OTHER INFORMATION: CNGB3
US-10-978-282-14

Query Match 76.0%; Score 3217; DB 5; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.1e-226;
Matches 615; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 195 MPEYELKIKIPNSIDSYTDRLYLWLLVLTAYNNWCFPLRLVFPYQADNIHYWL 254
DB 1 MPEYELKIKIPNSIDSYTDRLYLWLLVLTAYNNWCFPLRLVFPYQADNIHYWL 60
QY 255 IADIICDIYLYDMLFIQRLQVRGDIIVDSNELRKHRTSTKFLQDVASIIPEDICY 314
DB 61 IADIICDIYLYDMLFIQRLQVRGDIIVDSNELRKHRTSTKFLQDVASIIPEDICY 120
QY 315 LFFGFNPMFRANRMLKYTSFFFNHLSIMDKAYIYRVIRTTGYLLFILHINACYYYWA 374
DB 121 LFFGFNPMFRANRMLKYTSFFFNHLSIMDKAYIYRVIRTTGYLLFILHINACYYYWA 180
QY 375 SNYEGIGTRWYVDGEGNEYLRCYYWAVRTLITIGLPEPQTLFEIVFOLLNPFSGVFVF 434
DB 181 SNYEGIGTRWYVDGEGNEYLRCYYWAVRTLITIGLPEPQTLFEIVFOLLNPFSGVFVF 240
QY 435 SSLIGQMRDVI GAATANQYFRACMDTTIAYMNNYSIPKLQKRVRTWYETWDSORMLD 494
DB 241 SSLIGQMRDVI GAATANQYFRACMDTTIAYMNNYSIPKLQKRVRTWYETWDSORMLD 300
QY 495 ESDLLKTLPTTVQALALAIYVNFISIISKVDLFGKCDTQMIYDMLRLKSLVLYLPGDFVCKK 554
DB 301 ESDLLKTLPTTVQALALAIYVNFISIISKVDLFGKCDTQMIYDMLRLKSLVLYLPGDFVCKK 360
QY 555 GETGKEMYYIKHGEVQVLGPDGTQVLVTLKAGSVFGEISLLAAGGNNRTANVVAHGFA 614
DB 361 GETGKEMYYIKHGEVQVLGPDGTQVLVTLKAGSVFGEISLLAAGGNNRTANVVAHGFA 420
QY 615 NLTLDDKKTQELIVHPDSEIRILMKKARVLLKQAKTAEATPPKDLALLFPKSETPK 674
DB 421 NLTLDDKKTQELIVHPDSEIRILMKKARVLLKQAKTAEATPPKDLALLFPKSETPK 480
QY 675 LFKTLGGTGKASLARLLKLRQAAQKENSGBEGEKENEDKOKENEDK 734
DB 481 LFKTLGGTGKASLARLLKLRQAAQKENSGBEGEKENEDKOKENEDK 540
QY 735 KENEDKDKGREPBKPLDRPECTASPIAVBEEPHSVRRTVLPRTGTSQSLSIISMAPSAG 794
DB 541 KENEDKDKGREPBKPLDRPECTASPIAVBEEPHSVRRTVLPRTGTSQSLSIISMAPSAG 600
QY 795 GEEVLITIEVKEKAKQ 809
DB 601 GEEVLITIEVKEKAKQ 615

RESULT 4
US-10-978-282-12
Sequence 12, Application US/10978282
Publication No. US20050221426A1
GENERAL INFORMATION:
APPLICANT: YAO, Yong
APPLICANT: CAO, Liang
APPLICANT: LU, Jianming
APPLICANT: LILORENTE, Isabel
TITLE OF INVENTION: Novel Cell-Based Assays Employing Voltage and Calcium Dyes
FILE REFERENCE: 062614-5002-US
CURRENT APPLICATION NUMBER: US/10/978,282
CURRENT FILING DATE: 2004-11-01
PRIOR APPLICATION NUMBER: US 60/589,012
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: US 60/515,442

PRIOR FILING DATE: 2003-10-30
PRIOR APPLICATION NUMBER: US 10/087,217
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/330,663
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 1245
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)-(1245)
OTHER INFORMATION: CNGB1
US-10-978-282-12

Query Match 46.1%; Score 1952; DB 5; Length 1245;
Best Local Similarity 46.4%; Pred. No. 1.3e-133;
Matches 405; Conservative 121; Mismatches 237; Indels 110; Gaps 18;

QY 14 IGENNENEQSSRRNEEGSHPSNQSOTTAQE--ENKGE---EKSUKTKTPTVTSSEPHNTN 69
DB 403 VGEBAKKEAEKAE 462
QY 69 IQDK-----LSKNSSGDLTTNPDPOAAEPTGTVPQEKMDPKCEGPN----- 112
DB 463 VEDTDADSCPLMAEENPPS--TVLPPSPAKSDTLIVPSSASGTHRKKLPLSEDEAEELK 520
QY 113 --SPQKRP-----PAAP-----VINEYADAOLHNLVKMRORTALY 146
DB 521 ALSPAESPVVWSDPTTTPKDTGQDRAASTASTNSAIIND----RLQELVKLFKERTKV 576
QY 147 KKKLVGEGDLS----SPEASPTAKPTAVPPVKESDDKPT--EHYRLLLFKVKKMPLETEY 200
DB 577 KEKLDIPDVTSDSESPKSPAKKAPPAPOTKPAEAEPEVEEHEHYCDMLCKFKHRPWKKY 636
QY 201 LKRIKLPNSIDSYDRLYLWLLVLTAYNNWCFPLRLVFPYQADNIHYWLIADIIC 260
DB 637 ---QPPQSIDPLTNJMYLVLFVVMWNNWCWLIPIVRWAPYQPTPDNIHHWLLMDYLC 692
QY 261 DIILYDMLFIQRLQFVRGGDIIVDSNELRKHRTSTKFLQDVASIIPFIDICYLPFGFN 320
DB 693 DLIFUDITVQTRLOFVRGGDIITDKDMRNLYLSRRFKMDLLSLLPLDFLYLKGVN 752
QY 321 PMFRANRMLKYTSFFFNHLSIMDKAYIYRVIRTTGYLLFILHINACYYYWASNYEGI 380
DB 753 PLLRLPRLCKYWAFFEFNSRLESILSKAYVYRVIRTTAVLTYLSHLNSCLYYWASAYOGL 812
QY 381 GTTRWYVDGEGNEYLRCYYWAVRTLITIGLPEPQTLFEIVFOLLNPFSGVFSSLIQ 440
DB 813 GSTHWYVDGVGNSYIRCYFAVKTLITIGLPPKTLFEIVFOLLNPFSGVFASFVNIQ 872
QY 441 MRDVI GAATANONYFRACMDTTIAYMNNYSIPKLQKRVRTWYETWDSORMLDESLLK 500
DB 873 MRDVGAAGTAGQTYRSCMDSTVKYMNFKIPKSVQNRVKTWYETWHSOGLMDESELV 932
QY 501 TLPTTVQALALAIYVNFISIISKVDLFGKCDTQMIYDMLRLKSLVLYLPGDFVCKKEIGKE 560
DB 933 QLPDKMRLDLAIDVNYIVSKVALFOGCDRQMIQFDMKLRLRSVVYLPNDVYCKKKEIGRE 992
QY 561 MYIIKHGEVQVLGPDGTQVLVTLKAGSVFGEISLLAAGGNNRTANVVAHGFAANLLTLD 620
DB 993 MYIIQAGQVQLGPDGKSVLTLKAGSVFGEISLLAAGGNNRTANVVAHGFTNLPLD 1052
QY 621 KKTLOELVHYPSERILMKKARVLLKQAKTAEATPPKDLALLFPKKEETPKLFTLL 680
DB 1053 KDLNLEILVHYPSQKLLRKKARMLRSNNK-----PKEEKSVLIIPPRAGTPKLFWAAL 1107
QY 681 GGTGKAS-----LARLLKLRQAAQKENSGBEGEKENEDKOKENEDK 728
DB 1108 AMTKMGKGKAGKGLAHLARLKEALAEAAKQOEL----VEQAKSSODVKEGESAAP 1164

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QY 729 ENEDKGKE-NEDKDKGREPERK-----LDRPECTASPIAVEREPEHSVRTVLP 776
Db 1165 DQHTPKAATDPPAPRTPEPPGSPPPASLGRPEGBGA-EPEEHSVR----- 1218
QY 777 RGTSRQSLIISMAPSAEGGEEVLTIEVKEKAKQ 809
Db 1219 -----ICWSPGPEGEQILSVKMPPEREE 1242

RESULT 5
US-10-450-763-57830
; Sequence 57830, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CI23/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 57830
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (387)..(411)
; OTHER INFORMATION: Cyclic nucleotide-binding domain proteins domain identified
; OTHER INFORMATION: by eMATRIX, accession number BL00888B, p-value=9.143e-16, raw score
; OTHER INFORMATION: of 14.79
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (133)..(349)
; OTHER INFORMATION: Transmembrane region cyclic Nucleotide G domain identified by
; OTHER INFORMATION: Pfam, accession name CNG_membrane, E-values=2.4e-92, Pfam score of
; OTHER INFORMATION: 320.2
US-10-450-763-57830

Query Match 42.1%; Score 1781.5; DB 5; Length 652;
Best Local Similarity 55.3%; Pred. No. 1.6e-121;
Matches 343; Conservative 87; Mismatches 143; Indels 47; Gaps 7;

QY 214 TDRLLMLLLVTLAYNNWCNFIPLRLVFPYQADNIHNLADIICDIYLYDMLFIQP 273
Db 53 TDLMTVLMFFVMAWNNCWLPVRWAFYQTPDNIHHLMDVLYCDLIYFLDITVQT 112
QY 274 RLQFVRGGDIIVDSNELRKHYSSTKFDLVAISIIPDFICYLFFGNPMFRANRLKYTS 333
Db 113 RLQFVRGGDIITDKDMRNLYKSRFRKMDLSLLPLDFLYLKVGVPNLLRPLRCLKYMA 172
QY 334 PFEFNHLESIMDKAVIVRITGTGLFILHINACVYVWASNYGIGTTRVWYDGE 393
Db 173 PFEFNRLLESILSKAYVIRVITAYLLSLHNSCLYYWASAYQGLGTHWYDGVGNS 232
QY 394 YLRCYVAVRTLITIGLPEPOTLFEIVFQLLNFFSGVVFVSSLIGQMRDVIIGAATANQ 453
Db 233 YIRCYFAVAKTLITIGLPPDKTLFEIVFQLLNFTGVFAFVSMIGQMRDVVGAATAGT 292
QY 454 YFRACMDTIAWNNYSIPKLVOKRVTYEYTWDSQRMDSLLKTLPTTVQLALAI 513
Db 293 YRSCMDSTVKMNFYKIPKSVQNVKTYEYTWHSQGLMDESLMVQLPDKRDLAI 352
QY 514 VNFSIISKVDLPFGCDTOMIYDMLRLKLSVLYLPGDFVCKGKEIGKEMVIIKHGVOVLG 573
Db 353 VNYNIVSKVALFQGCDDROMIFDMLKRLRSVVLYPNDYVCKGKEIGREMYIIQAGQVVLG 412
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QY 574 GPDGPKVLVTLKAGSVFGEISLLAAGGNNRRTANVVAHGAFANLLTLDKKTLOEILVHYPD 633
Db 413 GPDGKSVLVTLKAGSVFGEISLLAVGGNNRRTANVVAHGFTNLFLDKKDLNEILVHYPE 472
QY 634 SERILMKKARVLLKOKAKTAEATPRKDLALLFPPEKETPKLFTKLLGGTGKAS----- 687
Db 473 SOKLLRKARRMLRSNNK-----PKEKSVLILPRACTPKLFNAALAMTKMGMGKGAGK 527
QY 688 -----LARLLKREOAAOKKENSEGEGEKENEDKOKENEDKKE-NEDK 740
Db 528 GKLAHLRLARLKEALAEAAKHEEL-----VEQAKSODVKGECSAAPQOHTHPKEAATDP 584
QY 741 DKGREPEEKPLDRPECTASPIAV-----EEPHSVRRTVLPRTGTSRQSLISMA 789
Db 585 PAPRTPEPP-GSPDSSPPASLGSGEGEESGPAEPESHSVR- 809
QY 790 PSAEGGSEVLTIEVKEKAKQ 809
Db 630 PGPEPGEQILSVKMPPEREE 649

RESULT 6
US-11-097-143-26427
; Sequence 26427, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL000728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26427
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: DROSOPHILA
US-11-097-143-26427

Query Match 26.1%; Score 1103; DB 6; Length 1037;
Best Local Similarity 33.4%; Pred. No. 1.5e-71;
Matches 243; Conservative 153; Mismatches 255; Indels 76; Gaps 13;

QY 16 ENNENEQSSRRNEGSHPSNQSQTTAQ-----EENKGEESLTKSTPTVTSSEPHNTI 69
Db 276 EEEEEKSSPLHOVESQDVDEQDVQICYNESPELONEDRNETORTPSINESEIVAV 335
QY 70 QDKLSKKNSSGDLTTNPDQNAAEPTGTVPQEKMDPGKEGPNSPONKPPAAPVINEYAD 129
Db 336 DEPDTEMNSDVD---HRKFPSSA---GSLDSQGO-----QFLR 366
QY 130 AOLHNLVKRMQORTALYKKLVGDLSSPEASPOKATPVAVPVKESDDKTEHYRLLW 189
Db 367 DQVRHLVRRRTARANKVKSRI---ELPTTSSSTSVSSPPTKSLHSP-QH----- 416
```

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QY 190 PKYKMPLETKRIKL-----PNSIDSYTD-----RLYLWLLLVTLA 228
Db 417 -KVLVPAGQPHRGLFEADTPRSNVMLCSSLGANDERTLDPQGIYISWLCVSL 475
QY 229 YNWNCFIDRLVPEYOTADNIHYMLIADIIDIIYLYDMLFIQPLQFVRGDDIIVDSN 288
Db 476 FLYNAWVILRASFPQTKENTINWILACDFCADIYLLDVFFPKHVMYLFEGFWKKN 535
QY 289 ELRKHYRTSTKFOLDVASIIPEDICYLFFGPMF-RANRMLKYTSFFEFNHHLESIMDK 347
Db 536 LTRKNTYRKLOPKDLALLPLELLYFKLTQAVWLRFPRFKIQSFWEVFRLLDRVSS 595
QY 348 AYIRVIRTTGYLLFILHINACYWASNYBEGITTRWYDSEGNLYLRCYVWAVTLIT 407
Db 596 PHFVRVAKTLTYLMYMIHTAALYYAYSQYGLQNRWVFSKGHPYVRCFAPATKTATS 655
QY 408 IGGLEPOTLPEIVFOLLNFFSIVFSSILIGOMRDVIGNATANYFRACDDDTIAYMN 467
Db 656 IGKNPKPERQGEYVFMVAMLGVFVALLIGQIRDIISTATNKGHEYLEDETLIYMR 715
QY 468 NTSIPKLVQKRVRTWYEYTDWSORMLDESLLKTLPTTVQLALAIWNFSIISKVDLPKG 527
Db 716 RLNLSEVQSRVQWFOFTWEQRTLDSENLDPALINLKTDAISVHIOTLSKVQLFAD 775
QY 528 CDTQMIYDMLRLKSVLYLPDGPVCKKGEIGKEMYYIKHGEVQVLGGPDGTRKVLTLKAG 587
Db 776 CBEALLRDLVLKRAVTFLPDGPVCKRGEVREMYIVKLQGVMMGSPSDVVVLTATLTEG 835
QY 588 SVFGEISLLAAGGNRTANVAHGAFANLLTLDKKTLOEILVHYVPSERILMKKARVLL- 646
Db 836 SVFGEISLLGADRRRTADVRSGYSLNLFVLSKSDNLNEVIAYYTAQAILKGRARQLMR 895
QY 647 KOKAKTAEATPPKDLAL-----LFPPK--EETPKLPKTLGGTGKASLARLLKLKREQA 699
Db 896 KNAREEREERARSALQADVIGNPKTPTAPKLLQTVIQALPESPASVAVLITRSGKR 955
QY 700 AQKENS 706
Db 956 MRRKQS 962

RESULT 7
US-10-450-763-35825
; Sequence 35825, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 35825
; LENGTH: 644
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (58)..(105)
; OTHER INFORMATION: kw TRANSCRIPTASE REVERSE II ORF2 domain identified by
; OTHER INFORMATION: eMATRIX, accession number DM01354V, p-value=1.000e-40, raw score
; OTHER INFORMATION: 12.97
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(644)
```

; OTHER INFORMATION: Xaa = X or * as defined in Table 2
US-10-450-763-35825

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Query Match 25.7%; Score 1088; DB 5; Length 644;
Best Local Similarity 100.0%; Pred. No. 9.9e-71;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 594 SLLAAGGNRRRTANVAHGAFANLLTLDKKTLOEILVHYVPSERILMKKARVLLKOKAKTA 653
Db 429 SLLAAGGNRRRTANVAHGAFANLLTLDKKTLOEILVHYVPSERILMKKARVLLKOKAKTA 488
QY 654 EATPPRKDLALLPPEKEETPKLPKTLGGTGKASLARLLKLKREQAQAOKKENSEGEEBEG 713
Db 489 EATPPRKDLALLPPEKEETPKLPKTLGGTGKASLARLLKLKREQAQAOKKENSEGEEBEG 548
QY 714 KENEDKQKENEKQKENEKQKENEKQKREPEEKPLDRPECTASPIAVEEPEHPSVRRT 773
Db 549 KENEDKQKENEKQKENEKQKENEKQKREPEEKPLDRPECTASPIAVEEPEHPSVRRT 608
QY 774 VLPRTSROSLLISMAPSASGEEVLTIEVKSKAKQ 809
Db 609 VLPRTSROSLLISMAPSASGEEVLTIEVKSKAKQ 644
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RESULT 8

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US-10-978-282-19
; Sequence 19, Application US/10978282
; Publication No. US20050221426A1
; GENERAL INFORMATION:
; APPLICANT: YAO, Yong
; APPLICANT: CAO, Liang
; APPLICANT: LU, Jianming
; APPLICANT: LLORENTE, Isabel
; TITLE OF INVENTION: Novel Cell-Based Assays Employing Voltage and Calcium Dyes
; FILE REFERENCE: 062614-5002-US
; CURRENT APPLICATION NUMBER: US/10/978,282
; CURRENT FILING DATE: 2004-11-01
; PRIOR APPLICATION NUMBER: US 60/589,012
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/515,442
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 10/087,217
; PRIOR FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/330,663
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human CNGA and CNGB consensus sequence
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(821)
; OTHER INFORMATION: Xaa = any naturally occurring amino acid
US-10-978-282-19
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Query Match 24.9%; Score 1052.5; DB 5; Length 821;
Best Local Similarity 38.6%; Pred. No. 5.6e-68;
Matches 227; Conservative 97; Mismatches 205; Indels 59; Gaps 6;

QY 205 KLPNSIDSYTDRLYLLWLLLVTLAYNNWNCWFILRLVFPYQOTADNIHYMLIADIICDIY 264
Db 256 KLLXVIDPSCDXLYLLWLFXIALPVNNWCLLVARACFPDLQSDYLYHVLVDVSDVY 315
QY 265 LYDMLFIQPLQFVRGDDIIVDSNEILRKHRYRTSTKTFOLDVASIIPDICYLFFGPN-PMF 323
Db 316 LLDMXFVRTGTGEOLGLLVVDNKLNNYKTTLQFKLDVASLIPTDLYLVKVGXNYPEV 375
QY 324 RANRMLKYTSFFEFNHHLESIMDKAYIYRVIRTTGVLILLFILHINACYWASNYEGIGTT 383
```


Db 1 LPEIVFOLLNNTYGVAFSPVMIGQMRDVVVGAAATACQTYTTRSCMDSTVKVMNFYKIPKSVQ 60
QY 477 KRVRTWYETWDSQRLMDESLLKTLPTTVQLALADVNFISIKVDLFGCDTQMIYDM 536
Db 61 NRKVTWYETWHSQGLMDESELVQLPDKMRDLALDVNYSKVALFQGCDCRQMIYDM 120
QY 537 LLRLKSVLYLPDGFVCKKGEIGEMKIIKHGEVQVLLGGPDGTVKLVTLKAGSVFGEISLL 596
Db 121 LKRLSVLYLPNDYVCKKGEIGEMKIIKHGEVQVLLGGPDGTVKLVTLKAGSVFGEISLL 180
QY 597 AAGGNRRRTANVAVHGFANLLTLDKKTQLQELVHYPDSEIRILMKKARVLLKQAK 651
Db 181 AVGGNRRRTANVAVHGFANLLTLDKKTQLQELVHYPDSEIRILMKKARVLLKQAK 235

RESULT 11

US-10-189-507-7
; Sequence 7, Application US/10189507
; Publication No. US20030228633A1
; GENERAL INFORMATION:
; APPLICANT: ZOLLER, MARK
; APPLICANT: XU, HONG
; APPLICANT: STASZEWSKI, LENA
; APPLICANT: MOYER, BRYAN
; APPLICANT: PROMIN, ALEX
; APPLICANT: ADLER, JON ELLIOT
; APPLICANT: SERVANT, GUY
; APPLICANT: CALLAMARAS, NICHOLAS
; TITLE OF INVENTION: EXPRESSION OF FUNCTIONAL HUMAN OLFACTORY CYCLIC
; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
; TITLE OF INVENTION: SMELL MODULATORS
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/189,507
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,140
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,154
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 7
; LENGTH: 237
; TYPE: 'PRT'
; ORGANISM: Rattus sp.
US-10-189-507-7

Query Match 21.3%; Score 902; DB 4; Length 237;
Best Local Similarity 72.3%; Pred. No. 1e-57;
Matches 170; Conservative 30; Mismatches 35; Indels 0; Gaps 0;
QY 417 LPEIVFOLLNNTYGVAFSPVMIGQMRDVVVGAAATACQTYTTRSCMDSTVKVMNFYKIPKSVQ 476
Db 1 LPEIVFOLLNNTYGVAFSPVMIGQMRDVVVGAAATACQTYTTRSCMDSTVKVMNFYKIPKSVQ 60
QY 477 KRVRTWYETWDSQRLMDESLLKTLPTTVQLALADVNFISIKVDLFGCDTQMIYDM 536
Db 61 NRKVTWYETWHSQGLMDESELVQLPDKMRDLALDVNYSKVALFQGCDCRQMIYDM 120
QY 537 LLRLKSVLYLPDGFVCKKGEIGEMKIIKHGEVQVLLGGPDGTVKLVTLKAGSVFGEISLL 596
Db 121 LKRLSVLYLPNDYVCKKGEIGEMKIIKHGEVQVLLGGPDGTVKLVTLKAGSVFGEISLL 180
QY 597 AAGGNRRRTANVAVHGFANLLTLDKKTQLQELVHYPDSEIRILMKKARVLLKQAK 651
Db 181 AVGGNRRRTANVAVHGFANLLTLDKKTQLQELVHYPDSEIRILMKKARVLLKQAK 235

RESULT 12

US-09-842-758-75
; Sequence 75, Application US/09842758
; Publication No. US20030083244A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Fernandes, Elma R
; APPLICANT: Gerlach, Valerie
; APPLICANT: Shinkets, Richard A
; APPLICANT: Maiyankar, Uriel M
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Zerhusen, Bryan D
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E
; APPLICANT: Gangolli, Esha A
; APPLICANT: Smithson, Glenda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R
; APPLICANT: Taupier, Raymond J
; APPLICANT: Grosse, William M
; APPLICANT: Edward, Szekeres S
; APPLICANT: Alsobrook II, John P
; TITLE OF INVENTION: No. US20030083244A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 15966-783
; CURRENT APPLICATION NUMBER: US/09/842,758
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/200,158
; PRIOR FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 60/200,613
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,780
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/201,006
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,007
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,236
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,238
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/201,186
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: 60/201,474
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/201,508
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 60/220,591
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: 60/232,678
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 60/263,217
; PRIOR FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: 60/265,160
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-842-758-75

Query Match 20.1%; Score 850; DB 3; Length 694;
Best Local Similarity 30.0%; Pred. No. 3e-53;

Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPSNQSQTTAAEENKGEESKLTSTPTVSEEPHTNIQDKLSKKNSSGDLTTNP 86

Db 5 NTQYSHPS-----RTHLKVK-----TSDRLNRAENGLSRAHSSSEETS-- 43

QY 87 DPONAAEPTGTVPQKEMDPGKGNPSQNKPPAAPVINEYADAOLHNLVKRMRQRTALY 146

Db 44 ---SVLPQ-GIANETRGADSGGSGFTGQ-----GIARLSRLIFLLRRWAARH 87

QY 147 KKLVGDLSSP-----EASPTAKPTAVPPVKESDDKPTBHYHYRLLWFKVKKMP 197
DB 88 VHQDQGPDPDFRFRGAELKEVSSQESNAQNVGSEPADRG-----RSAW-----PL 136
QY 198 -----TEYLKRIKLPNSI-DSYTDRLVLLMLLVTLAYNNWCWPIPLRLVFPYOT 246
DB 137 AKCNTNTSNTTEEEKTKKDAIIVDPSSNLYRMLTAIALPVFNWYLLICRACFDELQ 196
QY 247 ADNIHYMLIADIICDIYLYDMLFIQPRQLQVRGGDIIVDSNELRKHYRTSTKTFOLDVAS 306
DB 197 SEYLMMLVLDYSADVLYVLDV-VRARTGFLEQGLMVSDTNRLWQHVKYTKTTQFKLDVLS 255
QY 307 IIPFDICVLFQFN-PMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYLLFIH 365
DB 256 LVPTDLAYLVKVTNYPEVRFNRLKFSRLEFFDRTETRTNYPNMFRLGNLVLYLIIH 315
QY 366 INACVYVWASNYEGIGTRWYVDG-----EGNEYLRCYWAVRITLITIGGLEPOTL 417
DB 316 WNACIYFAISKFIGTDSWVYPNISIPHGRLSRKYIYSLWSTLTTLTTIGETPPVKD 375
QY 418 FEIVPOLLNFFSGVVFSSLIQMRDVI GAATANQNYFRACDDTTIAYNNYSIPLKVOK 477
DB 376 BEYLVFVWDFLVGLVIFATIVGVSMISNMNASRAEFOAKIDS IKQYMPRKVTKOLET 435
QY 478 RVRTWYETWDSQRMDESLDKTLPTTVQLALAI DVNFSIISKVDLFKGCOTMIYDML 537
DB 436 RVIRWFDVLMANKTVDEKVLKSLPKLKAIAINVHLDTLKVRIFQDCEAGLLVELV 495
QY 538 LRLKSVLVLPDGVCKKGIGKEMYYIHKHGVQVVGDPGTVKLVTLKAGSVFGEISLLA 597
DB 496 LKLRTPVSPGDIYCKKGDIGKEMYYINEGLAVV-ADGVTQFVLSGSGYFGEISILN 554
QY 598 AGG---GNRRRTANVVAHGFANLLTLDKKTLOEILVHYPDSERILMKKAR-VLLKOK--A 650
DB 555 IKGSKSGNRRRTANIRSIGVSLFCLSKDLMALTEYPEAKKALEEGRQILMKONLIDE 614
QY 651 KTAETATPRKDALILFPPEETPKLFTLLGGTGKASLARLL-----KLRQAAQAK 702
DB 615 ELARAGADPKDL-----EKEVEQLGSSL--DTLQTRFARLLAEYNAQTMKMKORLSOLE 666
QY 703 KENSEGEE---EGKENEDKOKENEDKOK 728
DB 667 SQVKGSGDKPLADGEVPGDATK-TEDKQK 694

RESULT 13

US-09-855-828-14
; Sequence 14, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855,828
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CNGAL
US-09-855-828-14

Query Match

Best Local Similarity 20.1%; Score 850; DB 3; Length 694;

Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPNQSOQTAAQENKGEESKLTKTSTPVTSSEPHNTIQDKLSKSNSSGDLTTNP 86
DB 5 NTQYSHPS-----RTHLKVK-----TSRDLNRAENGLSRAHSSEETS 43
QY 87 DPQNAAEPTGVPEOKEMDPGKEGPNSPONKPPAAPVINEYADAOLHNLVKRMORTALY 145
DB 44 ---SVLQP-GIAMESTRGLADSGQSFTCQ-----GIARLSRLIFLLRRWAARH 87
QY 147 KKLVGDLSSP-----EASPTAKPTAVPPVKESDDKPTBHYHYRLLWFKVKKMP 197
DB 88 VHQDQGPDPDFRFRGAELKEVSSQESNAQNVGSEPADRG-----RSAW-----PL 136
QY 198 -----TEYLKRIKLPNSI-DSYTDRLVLLMLLVTLAYNNWCWPIPLRLVFPYOT 246
DB 137 AKCNTNTSNTTEEEKTKKDAIIVDPSSNLYRMLTAIALPVFNWYLLICRACFDELQ 196
QY 247 ADNIHYMLIADIICDIYLYDMLFIQPRQLQVRGGDIIVDSNELRKHYRTSTKTFOLDVAS 306
DB 197 SEYLMMLVLDYSADVLYVLDV-VRARTGFLEQGLMVSDTNRLWQHVKYTKTTQFKLDVLS 255
QY 307 IIPFDICVLFQFN-PMFRANRMLKYTSFFEFNHLESIMDKAYIYRVIRTTGYLLFIH 365
DB 256 LVPTDLAYLVKVTNYPEVRFNRLKFSRLEFFDRTETRTNYPNMFRLGNLVLYLIIH 315
QY 366 INACVYVWASNYEGIGTRWYVDG-----EGNEYLRCYWAVRITLITIGGLEPOTL 417
DB 316 WNACIYFAISKFIGTDSWVYPNISIPHGRLSRKYIYSLWSTLTTLTTIGETPPVKD 375
QY 418 FEIVPOLLNFFSGVVFSSLIQMRDVI GAATANQNYFRACDDTTIAYNNYSIPLKVOK 477
DB 376 BEYLVFVWDFLVGLVIFATIVGVSMISNMNASRAEFOAKIDS IKQYMPRKVTKOLET 435
QY 478 RVRTWYETWDSQRMDESLDKTLPTTVQLALAI DVNFSIISKVDLFKGCOTMIYDML 537
DB 436 RVIRWFDVLMANKTVDEKVLKSLPKLKAIAINVHLDTLKVRIFQDCEAGLLVELV 495
QY 538 LRLKSVLVLPDGVCKKGIGKEMYYIHKHGVQVVGDPGTVKLVTLKAGSVFGEISLLA 597
DB 496 LKLRTPVSPGDIYCKKGDIGKEMYYINEGLAVV-ADGVTQFVLSGSGYFGEISILN 554
QY 598 AGG---GNRRRTANVVAHGFANLLTLDKKTLOEILVHYPDSERILMKKAR-VLLKOK--A 650
DB 555 IKGSKSGNRRRTANIRSIGVSLFCLSKDLMALTEYPEAKKALEEGRQILMKONLIDE 614
QY 651 KTAETATPRKDALILFPPEETPKLFTLLGGTGKASLARLL-----KLRQAAQAK 702
DB 615 ELARAGADPKDL-----EKEVEQLGSSL--DTLQTRFARLLAEYNAQTMKMKORLSOLE 666
QY 703 KENSEGEE---EGKENEDKOKENEDKOK 728
DB 667 SQVKGSGDKPLADGEVPGDATK-TEDKQK 694

RESULT 14

US-10-345-680-26
; Sequence 26, Application US/10345680
; Publication No. US20030148394A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Silos-Santiago, Immaculada
; APPLICANT: Venkateswarlu, Karicheti
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,
; TITLE OF INVENTION: 12303, 985, 13237, 13601, 18926, 318, 2038 OR 6351 MOLECULES.
; FILE REFERENCE: MPI02-012P1RM, OMNI
; CURRENT APPLICATION NUMBER: US/10/345,680
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US 60/349,511
; PRIOR FILING DATE: 2002-01-18
; PRIOR APPLICATION NUMBER: US 60/360,500
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/365,041

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; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/374,063
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/403,468
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/414,262
; PRIOR FILING DATE: 2002-09-27
; PRIOR APPLICATION NUMBER: US 60/419,986
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/423,809
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: US 60/429,797
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo Sapiens
; US-10-345-680-26

Query Match      20.1%; Score 850; DB 4; Length 694;
Best Local Similarity 30.0%; Pred. No. 3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPSNQSQQTTAQEENKGEKSLKTKSTPTVTEEPHTNIQDKLSKNSSGDLTTNP 86
DB 5 NTQYSHPS-----RTHLVK-----TSDRDLNRAENGLSRAHSSEETS-- 43
QY 87 DPQNAEPTGTVEQKEMDPGKGNPQNKPPAAVINEYADAQLHNLVKRMQRTALY 146
DB 44 ---SVLQP-GIAMETRGADSGGSGFTGQ-----GIARLSRLIFLLRWAARH 87
QY 147 KKKLVGDLSSP-----EASPTAKPTAVPPVKESDDKPTHEHYVRLMLFPKVKMPL 197
DB 88 VHQDQGPSPPDRFGAELKEVSSQESNAQNVGQEPADRG-----BSAW-----PL 136
QY 198 -----TEYLKRIKIPNSI-DSYDRLYLMLLLVTLVANNWCNFIPLRLVPPYOT 246
DB 137 AKCNTNTSNNTEBEKTKKDAIVDPSSNLYVRLMTALPVPVYNNYLLICRACFELQ 196
QY 247 ADNIHWLADIICDIILYDMLFIQPRQFVVGDIIVDSNELRKHVTSKTFOLDVAS 306
DB 197 SEYLMWLVLDSADLYLDVL-VRARTGFLQGLMVSDTNRLWQHYKTTQFKLDVLVS 255
QY 307 IIPFDICYLFFGFN-PMFRANRLKYSTPEFNHLESIMDKAYIVRVIRTTGCLFILH 365
DB 256 LVPTDLAYLKVGTYNPEVRNLLKFSRLPEFDRTETRTNYPNFRIGNLVLYILIIH 315
QY 366 INACVYMASNYEGIGTTRWYDG-----EGNEYLRCYYWAVRTLITIGLPEPOTL 417
DB 316 WNAIVFAISKFTIGFTDSWVYPNISIPHGRLSRKYIYSLYSLTTLTIGETPPVKD 375
QY 418 FEIVFQLLNFFSGVFFSSLIQMRDVIGNATANYFRACMDDTTAYMNNYSIPKLQVK 477
DB 376 EYLFVVDVFLVGLIFATTIVGVNISMNNAARAEFAQIDSIIKQYMQFRKVTQDLET 435
QY 478 RVRTWYBYTWSORMLDESLLKTLPTTVALAIDVNFPSIISKVDLPKGCDDTQMYDML 537
DB 436 RVIRWFDYLMANKTVDEKEVLSPLPKLKAETAINVHLDLTKKVRIFQDCEAGLLVELV 495
QY 538 LRLKSVLYLPDFVCKKGEIKEMYIIKHGEVQVLGGPDGKTVLVTLKAGSVFGEISLLA 597
DB 496 LKLRPTVSPGDYICKKDGKEMYIINEGKLAVV-ADDDVTQFVVLSDGSYFGEISILN 554
QY 598 AGG---GNRTANVAVGFANLLTLDKKTQLEILVHPDSDERILMKKAR-VLLKQK---A 650
DB 555 IKGSKGNRRNTAIRSIGYDLPCLSKDLDMEALTEYPEAKKALBEKGRQILMKDNLIDE 614
QY 651 KTEATPPRKDALLPPKETEPTKLFKTLVLLGGTGKASLARI-----KLKREOAAQK 702
DB 615 ELARAGADPKDL-----EBKVFOLGSSL---DTLQTRFARLLAEYNAQTMKQRLSQL 666
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QY 703 KENSEGEE---EGKENEDKOKENEDKOK 728
DB 667 SQVGGGDKPLADGEVPCDATK-TEDKQO 694

RESULT 15
US-10-174-333-75
; Sequence 75, Application US/10174333
; Publication No. US20040029220A1
; GENERAL INFORMATION:
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Fernandes, Elma R.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Zethusen, Bryan D.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Smithson, Glennda
; APPLICANT: Rastelli, Luca
; APPLICANT: MacDougall, John R.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Grose, William M.
; APPLICANT: Szekeres, Edward S.
; APPLICANT: Alsobrook, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Li, Li
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 15966-783 CIP1
; CURRENT APPLICATION NUMBER: US/10174,333
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 60/193,664
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 60/194,614
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: 60/195,063
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,066
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,067
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,068
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,069
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,070
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,510
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/219,855
; PRIOR FILING DATE: 2000-07-21
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: CuraSeqlist version 0.1
; SEQ ID NO 75
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-174-333-75

Query Match      20.1%; Score 850; DB 4; Length 694;
Best Local Similarity 30.0%; Pred. No. 3e-53;
Matches 225; Conservative 149; Mismatches 269; Indels 106; Gaps 22;

QY 27 NEEGSHPSNQSQQTTAQEENKGEKSLKTKSTPTVTEEPHTNIQDKLSKNSSGDLTTNP 86
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OM protein - protein search, using sw model

Run on: December 21, 2005, 19:54:15 ; Search time 13 Seconds
(without alignments)
443.837 Million cell updates/sec

Title: US-09-855-828-1
Perfect score: 4234
Sequence: 1 MFPSLTKNVKVPGENNEN.....PSAEGGEVLTIEVKEKAKQ 809

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 53982 seqs, 7132107 residues

Total number of hits satisfying chosen parameters: 53982

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New.*
1: /cgn2_6/prodata/2/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/prodata/2/pubpaa/US06_NEW_PUB pep.*
3: /cgn2_6/prodata/2/pubpaa/US07_NEW_PUB pep.*
4: /cgn2_6/prodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /cgn2_6/prodata/2/pubpaa/US09_NEW_PUB pep.*
6: /cgn2_6/prodata/2/pubpaa/US10_NEW_PUB pep.*
7: /cgn2_6/prodata/2/pubpaa/US11_NEW_PUB pep.*
8: /cgn2_6/prodata/2/pubpaa/US60_NEW_PUB pep.*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	818.5	19.3	690	6	US-10-613-744-19
2	484	11.4	261	6	US-10-613-744-18
3	317.5	7.5	1159	6	US-10-613-744-12
4	302.5	7.1	857	6	US-10-613-744-11
5	282.5	6.7	597	6	US-10-613-744-7
6	131.5	3.1	3375	7	US-11-044-111-23
7	124	2.9	447	6	US-10-793-626-2900
8	124	2.9	450	6	US-10-793-626-3226
9	117	2.8	57	6	US-10-613-744-38
10	116.5	2.8	410	6	US-10-821-234-912
11	113	2.7	4374	7	US-11-128-572-2
12	112	2.6	635	6	US-10-821-234-1573
13	109.5	2.6	2897	6	US-10-499-715-2
14	107	2.5	57	6	US-10-613-744-39
15	106.5	2.5	598	7	US-11-113-837-18
16	106.5	2.5	644	6	US-10-793-626-1436
17	106.5	2.5	665	7	US-11-113-837-19
18	105.5	2.5	440	7	US-11-108-172-1059
19	105	2.5	1618	6	US-10-984-645-2
20	104	2.5	567	6	US-10-485-517-216
21	104	2.5	635	7	US-11-113-837-16
22	104	2.5	877	6	US-10-485-517-200
23	103.5	2.4	482	6	US-10-821-234-1413
24	102.5	2.4	547	6	US-10-770-726-87
25	102.5	2.4	667	6	US-10-821-234-1477

26	102	2.4	1390	7	US-11-063-343-35	Sequence 35, Appl
27	101.5	2.4	4868	7	US-11-044-111-24	Sequence 24, Appl
28	101	2.4	769	6	US-10-485-517-401	Sequence 401, Appl
29	101	2.4	1116	6	US-10-485-517-238	Sequence 238, Appl
30	101	2.4	1117	6	US-10-485-517-206	Sequence 206, Appl
31	100.5	2.4	795	6	US-10-770-726-49	Sequence 49, Appl
32	100.5	2.4	1122	6	US-10-821-234-1657	Sequence 1657, Ap
33	100	2.4	559	6	US-10-793-626-1376	Sequence 1376, Ap
34	99.5	2.4	457	6	US-10-982-545-8	Sequence 8, Appl
35	99.5	2.4	457	6	US-10-982-545-13	Sequence 13, Appl
36	99.5	2.4	715	7	US-11-089-551A-47	Sequence 47, Appl
37	98.5	2.3	290	6	US-10-821-234-862	Sequence 862, Appl
38	98.5	2.3	550	7	US-11-113-837-17	Sequence 17, Appl
39	98.5	2.3	853	6	US-10-821-234-1110	Sequence 1110, Ap
40	97.5	2.3	499	6	US-10-508-263-94	Sequence 94, Appl
41	97.5	2.3	756	7	US-11-188-743-20	Sequence 20, Appl
42	97.5	2.3	828	6	US-10-501-039-2	Sequence 2, Appl
43	97	2.3	313	6	US-10-873-528-163	Sequence 163, Appl
44	97	2.3	1263	6	US-10-485-517-127	Sequence 127, Appl
45	97	2.3	2261	6	US-10-995-561-600	Sequence 600, Appl

ALIGNMENTS

RESULT 1

US-10-613-744-19
; Sequence 19, Application US/10613744
; Publication No. US2005027093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-19

Query Match	19.1%	Score	818.5	DB	6	Length	690
Best Local Similarity	30.0%	Pred. No.	1.2e-51				
Matches	221	Conservative	128	Mismatches	262	Indels	125
Gaps	22						
Qy	5	LTQVNVKPIGENNENQSSRRNEEGSHPS	-----NOSQOTTAAOENKGE	-----KSL	53		
Db	17	VTWPNVIVP	-----DIEKEIRRMENACACSFSDDDSDSAYTSESEENPHARGCSFYKSL	71			
Qy	54	KTKSTPTVTSSEPHNTIQDKLSKKNSSGDLTTPDPONAAEPTGTVPQEKMDPKCKGPN	113				
Db	72	R-KGQPSQREYLPGAIAIFNVNNS	-----NKD	-----QEPPEKKKKKKKKSKSDDKNE	121		
Qy	114	PQNKPAAPVINEYADAQLHNLVKNRQRTALYKXKLVGDLSSPEAS	POTAKTAPVPV	173			
Db	122	NKNDPE	-----KXKKKKKKKKKK	-----E	141		
Qy	174	KESDDKPTHEYRLWPKVKKMPLTEYLKRIKLPNSIDSYTDRLYLWLLVTL	---AYNW	231			
Db	142	EKSKDKKEH	-----KKEVVV	-----IDP-SGNTYYNWLFCITL	180		

Db 484 SHPGRIAVHYFKGW-FLIDMVAAPDL--LIFGSG-----SEELIGL 523
QY 345 MDKAYIYRVRTGYL-----LFIL-----HINACVYWAGNYE-----CI 380
Db 524 LKTBARLLRVRVARKLDYRSEYGAVALFLMCTFALIAHWLACIWAIGNMOPHMDSRI 583
QY 381 GTRRWV-----YDGE-----NEYLRCCYVAVRTLTIG-GLPEPOTLFEIVF 422
Db 584 G---WLHNLGDOQIGKPYNSGLGPGSIKOKYVVALYFTFSSLTSGVGNVSPNTSEKIF 640
QY 423 QLLNPFSGVVFSSLLIGOMRDVIGATANQNYFRACMDDTIAYMNNYSIPKLVQKVRW 482
Db 641 SICWMLIGSLMYASIFGNYSIAIQRYSCTARYHTQMLRVREIRPHQIPNLRQRLBEY 700
QY 483 YEYTWDSQRLMDESLLKTLPTTVQALALADVNFSIISKVDLFGKCDTQMIYDMLRLKLS 542
Db 701 FQAWSYTNGIDNNAVLKGFPECLQADICHLNRSLLQHCXPRGATKGLRALANKPKT 760
QY 543 VLYLPGDFVCKGKEIGKEMYIIKHGEVQVVGPDGKTKVLVTLKAGSVFGE-ISLLAAGG 601
Db 761 THAPPGDTLVHAGDLLTALYFISRGSEIIL---RGDWVAILGKNDIFGEPLNLYARPG- 816
QY 602 NRTANVAVHGFANLTLQKTLQELVHYPD 633
Db 817 -KSGDVRALTYCDLKHHRDDLLLELDVMPYE 847

RESULT 4

US-10-613-744-11
; Sequence 11, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Cation Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 857
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-613-744-11

Query Match 7.1%; Score 302.5; DB 6; Length 857;
Best Local Similarity 23.2%; Pred. No. 2.2e-14;
Matches 110; Conservative 91; Mismatches 226; Indels 47; Gaps 15;
QY 202 KRKLPSIDSYDRLYLLMLLLVTLAYNWCNCFIPLRLVF-----PYQTADNIHWYLI 255
Db 41 RVKLRFVVSYPYDKHYRIWEAFVLVAVYTAWSPEFGFLRKPRLPSITDNI---VN 97
QY 256 ADIICDIYLYDMFIQRIQFVRGGDIIVDSNELKHYRTSTKFDQDVASIIIPD----- 311
Db 98 AFFAIDIMTFVFGYLDKSTYL-----IVDRKQIAFKYLRWS-FLDLVSTIPSEAMR 151
QY 312 ICYLPFGFNPMFRANMLKYTSFPFENHLESIMDKAYIY-RVIRTGTYLLFILHINACV 370
Db 152 ISSOSYGLFNMLRWLRRLRRVGALFA---RLEKORNFNYFWRCALKVCVTLFAVHCACF 208

QY 371 YW-----ASNVEGIGTTRWVYDGESEYLRCCYVAVRTLTIG-CLPEPOTLFEIV 421
Db 209 YWYLAARNSNPACTWIGANVANFLEESLWMRYVVTSMYSITTLTVGYDGLHPVNTKEM 268
QY 422 FOLLNPFSGVVFSSLLIGOMRDVIGATANQNYFRACMDDTIAYMNNYS-----PKLVOK 477
Db 269 FDIYFMYLNLGTLAVLIGNMTNLVVHGTSTRTNFR---DTIOAASNFARHNLPPRLQD 324
QY 478 RV-RTWYETWDSQRLMDESLLKTLPTTVQALALADVNFSIISKVDLFGKCDTQMIYD 535
Db 325 QMLAHLCLKYRTDSEG-LQQOETLDALPKAIRSSISHFLYSLMDKVVLYFRGVSNDLLFQ 383
QY 536 MLRLKSVLYLPGDFVCKGKEIGKEMYIIKHGEVQVVGPDGKTKVLV-TLKAGSVFGEIS 594
Db 384 LVSEMAEYFPKPEDVILQNEAPTDFYILVNGTADLVVDVTGTESTIVREVKAGDIIGEIG 443
QY 595 LLAAGGNRRRTANVAVHGFANLTLQKTLQELVHYPDSEIRILMKKARVLLKO 648
Db 444 VLYC---RPQLFTVTRKLCQLLRNRTTFLNIQANVGDGTIIMNNLLQHLKE 494

RESULT 5

US-10-613-744-7
; Sequence 7, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Paramesicium tetraurelia
US-10-613-744-7

Query Match 6.7%; Score 282.5; DB 6; Length 597;
Best Local Similarity 23.3%; Pred. No. 3.8e-13;
Matches 118; Conservative 95; Mismatches 212; Indels 81; Gaps 23;
QY 178 DKPT-----BHYI-RLLNFKVKQKPLTEYL-----KRKLPSIDSYDRLYLLMLLLVTL 227
Db 98 EKPTGFGQGHFLNQTLLPLRKLTKLYKCYGKQKLMRPELASIWNWYIITIL----- 153
QY 228 AYNNWCNCFIPLRLVFVQVADNIHWYLIADIICDIYLYDMFIQRIQF-----VRGDI 283
Db 154 --NINVLVYSIKITAFKFDQSDQDFVQARQIIFDVLPSSVFM-LEILLKENTCYKGV 210
QY 284 IVDSNELKHYRTSTKFDQDVASIIIP-----FDICVLFPGFNPMFRANMLKYTSFPEF 337
Db 211 IENRYQIAKNYLSS-FFDFIVVIVFISRLFDQLVLDVI-----ILKVFQITKF 261
QY 338 NHLESIMDKAYIYRVI---RTTGY-LLFLHLNACVYVWASNYEGIGTTRWV-----YDG 389
Db 262 SRNLFORLELTAIQIVTDVLVGLGYTILAAAHFSACTIWFVLVSGTNPNDTSWIKAOIN 321
QY 390 EG--NEVLRCCYVAVRTLTIG-GLPEPOTLFEIVFOLLNPFSGVVFSSLLIGOMRDVIG 446
Db 322 EQWFNOYHLSLYSIITMTTIGYDITPQNLRRERVAVGMAISAVGVFGYSGINISYIA 381

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QY 447 AATANQNYFRACDDTIAMNNYSIPKLVQKRVRTWYETWDSQRMLESLLK---TLP 503
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
382 ENSRQFOIRTDNNLKFKIRIKINGINKHAEKIRKYFEYVWSDQMEDNDREVYKSEMP 441
QY 504 TTVQLALAIQVNFPSIISK-----VDLPKGCOTQMIYDMLRLKSVL-----YLP 550
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
442 KQLAEMKIDTNNKIQKNSFLVNNFS-----EQFLISLSKVLIEKYVPESTIYLVK 494
QY 551 ---VCKKGEIGKEMVIKIHGEVQ---VLGGPDGT-KVLVTLK-AGSVFGEISLLAAGGN 602
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
495 LINILQNDPSNYLXLSNGLSFSYITLNNKQQTIKVLETIKNEGAQFVLEFFQS---Q 551
QY 603 RRTANVVAHGFANLTLTKKTIQEIL 628
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
552 AYQVSCSKNQFSVVLKIDKRSQPMWII 577

RESULT 6
US-11-044-111-23
; Sequence 23, Application US/11044111
; Publication No. US20050272362A1
; GENERAL INFORMATION:
; APPLICANT: Chiang, Wen
; APPLICANT: Strasbourg, Gale
; APPLICANT: Lin, John
; TITLE OF INVENTION: Genetic Test for PSE-Susceptible Turkeys
; FILE REFERENCE: MSU-09308
; CURRENT APPLICATION NUMBER: US/11/044,111
; CURRENT FILING DATE: 2005-01-27
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 23
; LENGTH: 3375
; TYPE: PRT
; ORGANISM: Meleagris gallopavo
US-11-044-111-23

Query Match 3.1%; Score 131.5; DB 7; Length 3375;
Best Local Similarity 21.3%; Pred. No. 0.29;
Matches 109; Conservative 66; Mismatches 198; Indels 139; Gaps 22;

QY 322 MFRANMLKYTSFFFNHLESIMDKAYIRVIRTTGYLLFLHINACVYVWASVNEGIG 381
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2485 LFRLLQLCEGHNDPQNYLRTQTGNTTTTINIICTVDYLLRLQESISDFYV--YVSG-- 2540
QY 382 TTRWYVDGEGNEVLRCCYYWAVRTLITIGLPEPQTLFEIVFQLLNFFSGVFVFSILQOM 441
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2541 --KVIDEGOKR-----NFSKAMAVAKQVFNSL 2566
QY 442 RDVI-GAATANQNYF--RACMDDTIAYMNNYS--IPKLVQKRVRTWYETWDSQRMLES 496
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2567 TEYIQGPGTGNQQLSAHSRLWDVVGFLVFAHMMKLAQ-----DSSQIGLLK 2615
QY 497 DLLKTLPTVQLALAI-----DVNFSIISKV---DLFKGCOTQMI---YDMLRLKSVL-- 544
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2616 ELLDQKQMVVWMLLSLEGVNVNGTIARQVQVMPVNESSNVMTMLKFFDMFLKLRDIVAS 2675
QY 545 -----YL--PGSFVCKKGIGKEMVIKIHGEVQVLLGGPDGTKVLTCLKAGSVFGEISLLA 597
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2676 DAFRYVTDPRGLISKK--DFQKAMDSQKQY-----PSEVQFLJLSCSEADNEMIDVEA 2728
QY 598 AGGGRNRTANVVAHGFANLLTLDKKTLQBIHVHPDSEIRILMKKARVLLKQAKTAEATP 657
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2729 FVGRSQEPARDIGFNVAVLLT-----NLAHVHPDQRL-----RTFLEQAASILE--- 2773
QY 658 PKDLALLFPKPEETPKFLTKLGGTGKASLARLL-KLKREQAOKKENSEGEGEBEGKE- 715
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2774 -----YRPFPLGRIEINGAARRIERLYFEISAANKAQWEMPQSDGKEV 2816
QY 716 NEDKOKENEDKOKENEDKOKREPEEKPLDRPE--CTASPIAVEEPEHPSVRT 773
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2817 VEPQKEBEEAAAEKADTENGEKGDGGAEGGPEVETPEKQOKASPPRERKEP----- 2870
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QY 774 VLPRGTSRQSLIISMAPSAEGGEEVLT-IEVK 804
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
2871 -----PPPEGAFETWTELEVO 2886

RESULT 7
US-10-793-626-2900
; Sequence 2900, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2900
; LENGTH: 447
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2900

Query Match 2.9%; Score 124; DB 6; Length 447;
Best Local Similarity 27.9%; Pred. No. 0.067;
Matches 48; Conservative 24; Mismatches 72; Indels 28; Gaps 6;

QY 662 LALLFPKPEETPKFLTKLGGTGKASLARLLKLKREQAOKKE----- 704
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MANLDERKKEITANLISKAQEAVERGDLLETARNLKADIDAQKREVEELQLSKEIASAPK 60
QY 705 NSEGGEEEGKENEKQ-----KENEKOKENEDKGENEDK-DKGREPEEKPLDRPECTA 758
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
61 QDEPPKDEGAEDNKDNGSGESENKPSDDPEGTSDEEKPDPAKPDCKPEETPE-Tp 119
QY 759 SPIAVEE--EPHSVRRTVLPRTGTSRQSLIISMAPSAEGGEEVLTIEVKEKAK 808
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
120 TIEKVEEPTBELKKEKDKKEGAKRSMAKLQNP--ETNEEILAFEQYMKSK 169

RESULT 8
US-10-793-626-3226
; Sequence 3226, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3226
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-3226

Query Match 2.9%; Score 124; DB 6; Length 450;
Best Local Similarity 27.9%; Pred. No. 0.067;
Matches 48; Conservative 24; Mismatches 72; Indels 28; Gaps 6;
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QY 662 LALLFPKBTPTKFKTLGGTGKASLARLLKLRQAAQKKS----- 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 1 MANLDERKKEIANLISKAQAVEKGDLETARNLKADIDAQKKEYBLEQLSKIEASAPK 60

QY 705 NSEGGEEGKENEKDK-----KENEDKOKENEDKGENEDK-DKGREPEKPLDRPECTA 758
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 61 QDEPPKDEGAVEDNKGNGSESEKPKSPDEFGTSDEKPDPAKPDKPRETE-TP 119

QY 759 SPIAVEE--EPHVSRRVTLPRGTSRSLIISMPSAEGGEEVLTIEVKEKAK 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 120 TIEKVEEPTTEELKKEKDKKGAKRSMKLNQNP--ETNEEILAFEQYMKSK 169

RESULT 9
US-10-613-744-38
; Sequence 38, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-38

Query Match 2.8%; Score 117; DB 6; Length 57;
Best Local Similarity 36.1%; Pred. No. 0.013;
Matches 22; Conservative 13; Mismatches 22; Indels 4; Gaps 1;

QY 393 EYLCRYWAVRTLITIGLPEPQLFEIVFOLLNFFSGVFFSSLIQMRDVGAATNQ 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 1 EYICLYWSTLTLTIGETPPVKNDEYLFVDFLIGLVIFATVGN----VGSMTSNM 56

QY 453 N 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 57 N 57

RESULT 10
US-10-821-234-912
; Sequence 912, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 912

QY 662 LALLFPKBTPTKFKTLGGTGKASLARLLKLRQAAQKKS----- 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 1 MANLDERKKEIANLISKAQAVEKGDLETARNLKADIDAQKKEYBLEQLSKIEASAPK 60

QY 705 NSEGGEEGKENEKDK-----KENEDKOKENEDKGENEDK-DKGREPEKPLDRPECTA 758
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 61 QDEPPKDEGAVEDNKGNGSESEKPKSPDEFGTSDEKPDPAKPDKPRETE-TP 119

QY 759 SPIAVEE--EPHVSRRVTLPRGTSRSLIISMPSAEGGEEVLTIEVKEKAK 808
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 120 TIEKVEEPTTEELKKEKDKKGAKRSMKLNQNP--ETNEEILAFEQYMKSK 169

RESULT 9
US-10-613-744-38
; Sequence 38, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: The Rockefeller University
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; TITLE OF INVENTION: Cation Channel Proteins, Mutant Prokaryotic Cation
; TITLE OF INVENTION: Channel Proteins, and Uses Thereof
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-613-744-38

Query Match 2.8%; Score 117; DB 6; Length 57;
Best Local Similarity 36.1%; Pred. No. 0.013;
Matches 22; Conservative 13; Mismatches 22; Indels 4; Gaps 1;

QY 393 EYLCRYWAVRTLITIGLPEPQLFEIVFOLLNFFSGVFFSSLIQMRDVGAATNQ 452
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 1 EYICLYWSTLTLTIGETPPVKNDEYLFVDFLIGLVIFATVGN----VGSMTSNM 56

QY 453 N 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 57 N 57

RESULT 10
US-10-821-234-912
; Sequence 912, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 912
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; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Query Match 2.8%; Score 116.5; DB 6; Length 410;
Best Local Similarity 24.0%; Pred. No. 0.21;
Matches 55; Conservative 29; Mismatches 102; Indels 43; Gaps 7;

QY 426 NFFSGVVFSSLIQMRDVIGAATANONFRACMDDTIAYMNN----- 468
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 177 DIFDAMFSVSFTAGE--TVIQQDEGDNFVVIDOGETDVVNVNNEWATSVGEGSGFGEAL 234

QY 469 -YSIPKLVOKRVRT-----WYEYTWDSQRMLEDSDLLKTLPTTVQLALADVNFSIISKVD 523
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 235 IYGPRAATVAKATNVKLMGIDRDSYRRILMGSTLKR-----KMYEEFUSKVS 283

QY 524 LFKGCDTQMIYDMLRLKSVLYLPFGDFVCKKGIGKEMVIIKHGEVQVLCGPDGTVKLV- 582
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 284 ILESKWERLTVADALEPVQFEDGOKIVVQEGPGEFFILLEGSAVLORRSENEEFVE 343

QY 583 --TLKAGSVFGEISLLAAGGNNR-RTANVVAHGAFANLLTLDDKKTLOEIL 628
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-912

Db 344 VGRLGPSDYFGEITALLM---NRPRATVVARGPLKCVKLDPRPRFVRL 388

RESULT 11
US-11-128-572-2
; Sequence 2, Application US/11128572
; Publication No. US20050266513A1
; GENERAL INFORMATION:
; APPLICANT: Boehringer Ingelheim International GmbH
; TITLE OF INVENTION: Method for identifying compounds that have the potential to inhibit
; TITLE OF INVENTION: activity of Myc
; FILE REFERENCE: Case 12-0231-PCT
; CURRENT APPLICATION NUMBER: US/11/128,572
; CURRENT FILING DATE: 2005-05-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4374
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-572-2

Query Match 2.7%; Score 113; DB 7; Length 4374;
Best Local Similarity 25.6%; Pred. No. 9;
Matches 33; Conservative 25; Mismatches 41; Indels 30; Gaps 4;

QY 635 ERLMKARVLLKOKAKTATAPPRKDALLFPKKEETPKLFTLLGGTGKASLARLLKL 694
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-572-2

Db 2379 EDVLMDEAPSNLSQ-ASTLQAN--REDSMNILPEDE----- 2412

QY 695 KRQAAQKENSEGEEGKENEKOKENEDKGENEDKDKGREPEKPLDR- 753
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-572-2

Db 2413 --BEHTQEEDESGSNEDEDSQDEEEEBEEDDQDEDEGDDDDDDGSEWELDED 2470

QY 754 -PECTASPI 761
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-572-2

Db 2471 YPDNWSPL 2479

RESULT 12
US-10-821-234-1573
; Sequence 1573, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
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; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1573
; LENGTH: 635
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1573

Query Match
Best Local Similarity 2.6%; Score 112; DB 6; Length 635;
Matches 51; Conservative 43; Mismatches 74; Indels 52; Gaps 10;

QY 577 GTKVLV-TLKAGSVFGEISLLAAGGNNRTANVAHGFAALLTLDKKTLQELVHPDSE 635
DB 17 GTKAFNEALQAGA---DISMIGQGVGFSAYLVA-----EKTIV--ITKHNDDQ 62
QY 636 RILMKKARVLLKQAKTATPPRKDLALLFPFKETPKLFTLLGGTGKASLARLLKLK 695
DB 63 YAWESSAGGSFTVRTDTGE--PMGRCTKVILHLKEDQTEYLE-----ERRIKEIVK-K 112
QY 696 REQ-----AAQKENSEGEEKEKEDKQKEDKQKEDK-----OK 735
DB 113 HSQFTGYPTLTFVEKERDKEVSDDEAEKEDKEEKEKEKESDKPETEDVGSDBEEK 172
QY 736 ENEDKDKGPREPKLID-----RPECTASPIAVEEHP 768
DB 173 KGGDKKKKKIKKIKYIDQELNKTKEIWRNPDDITNESY 212

RESULT 13
US-10-499-715-2
; Sequence 2, Application US/10499715
; Publication No. US20050250717A1
; GENERAL INFORMATION:
; APPLICANT: BENAYAHU, Dafna
; TITLE OF INVENTION: CHROMATIN REMODELING PROTEIN AS A MARKER EXPRESSED BY STROMAL PRO
; FILE REFERENCE: BENAYAHU=1.1 PCT
; CURRENT APPLICATION NUMBER: US/10/499,715
; CURRENT FILING DATE: 2004-06-21
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 2897
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-499-715-2

Query Match
Best Local Similarity 2.6%; Score 109.5; DB 6; Length 2897;
Matches 166; Conservative 138; Mismatches 290; Indels 345; Gaps 48;

QY 3 KSLTKVKN-VKIG--ENNENQSSRRNEEGSHPSNQSOQTAAQENKGEKSLTKSTP 59
DB 589 KEKTKIGKLIITLKKQKKNESDSEISDAEQPQHTLKQDSQKRSNRQIRKKYABD 648
QY 60 VTSEEPHTNIQKLSKNSGDL-----TTNPDQNA--EPTGTVPQKEMDFG 107
DB 649 IEGKQSEEVKGMKIKNSAPLPGEQPLQFLFENPSEDAIVDKILSSRTVKKKISPG 708
QY 108 KEGPNSQNKPPAAPVIN-----EVA-----DAQLNLVKNRQRTA 144
DB 709 -----VWIDTEEFVKYKNYSYLHCWATEBQLLKRIQKKIRKFLROA 754
QY 145 LYKKKLVEGDLSSPASPOTAKPTAPVPVKESDDKPTHEH---YRLLWFKVKKMPLEVL 201
DB 755 --QRAHFFADMBEFPNDPVEVDVLEVSFCEDKDTGEPVIYLVKVCSLPYEDSTWEL 812
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QY 202 K-----RIKLPS-----IDSYTD-----RLYLIL WLL 223
DB 813 KEDVDLAKTEEPEQLQASRPDTRRLDRPSPNIWKIDQSRDYKNGNQLREYQLEGLNWL 872
QY 224 LVTLAYNW---NCWFIPLRLVFPYQTADNIHYWLAD-----IICDIYLYDMLFIOP 273
DB 873 -----FNWYNRRNC-----ILADEMGLGKTIOSTIFLYEIL-----903
QY 274 RLQFVRGGDIIVDSNELRKHYRTSTKFDLDVASIIPFDICYLFFGFNPMFRANRMLKYTS 333
DB 904 -LTGIRGPFLLIAPLSTIANWEREFRTWTDINVV-----YHGLISRWMIQQYE 952
QY 334 PFEFNHLESIMDKAYIVRVIRTTGYLLFILHINACVYVWASNYEGIGITRVRWYDGE 392
DB 953 MY-FRDSQGRIRGAYRFOAIITT---PEMILGCGELNAIEW-----RCVIIDEAHR 1001
QY 393 -----EYLCRCYVAVRTLITIGGLPEPOTLFEIVFOLLNF-----FSGVFVFPSSL 438
DB 1002 LKNKCKLEGLKJMNLEHKVLLT--GTPLOQNTVEEL--FSLHLFLELPURFPSESTFMOEF 1054
QY 439 GQMRDVGAAATANQNYFRACDDTTIAYMNVSI PKLVOKRVRTWYEYTWDSORML DES 496
DB 1059 GDLK-----TEEQVKLOAILKPMML--RLKE-----DVEKKLAPKEE 1095
QY 497 DLLKTLPTTVQ---LALAIDVNFISIISKVDLPKGC---DTQMIYDMLRLKLSVLYLPGDF 550
DB 1096 TIEVELTNIQKKYVRAILEKNFSFLS-----KGAGQTNVPLNVTMELRCCNHP--- 1147
QY 551 VCKKGEIGKEMVILKHGEVOVLG-----GPDGT-----KVLVTLKA 586
DB 1148 -----YLIKGAEKILGEFRDTYNPAASDFHLQAMTQSAGKLVLDKILPKMKA 1196
QY 587 GS---VFGEISLLAAGGNNRTANVAHGFAALLTLDKKTLQELVH 630
DB 1197 GGHKVLIFSOM-----VRCLD--ILEDYLIHKRYLYERIDGRV 1232
QY 631 -----YDPSERILMKKARVLLKOKAKTAEATPPRKDLALLFP--PKEETP 673
DB 1233 RGNLRQAAIDRPSKPSDRFVPF---LLCTRAGLGIGINTAADTCIIFDSMDNPQNDIQ 1287
QY 674 KLFTKLLGGTGKA-SLARL-----LKLKREOAAQK---KENSEGGEHKG 733
DB 1288 AQARCHIRGONKAVKVVYLVTRNSYVEREMFRASLUGLDKAVLOSMSGRESNVGIG 1346
QY 714 KENEDKQKEDKQK-----ENEDKGE--NEDKOK 742
DB 1346 ---QLSKKEIEDLLRRGAYGAIMEDEEGSKFCEEDIDQ 1381

RESULT 14
US-10-613-744-39
; Sequence 39, Application US/10613744
; Publication No. US20050272093A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; TITLE OF INVENTION: Assays for Screening Compounds Which Interact With
; FILE REFERENCE: 018512-002901US
; CURRENT APPLICATION NUMBER: US/10/613,744
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: US/09/275,252
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: US 09/045,529
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/054,347
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: WO PCT/US99/06307
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 39
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 15:46:45 ; Search time 1330 Seconds
(without alignments)
12176.844 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 atgtttaatcgtgacaaa.....aagaaaagctgaagcaataa 2430

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_21.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002as.*
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8: Geneseqn2003as.*
9: Geneseqn2003bs.*
10: Geneseqn2003cs.*
11: Geneseqn2003ds.*
12: Geneseqn2004as.*
13: Geneseqn2004bs.*
14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2430	100.0	2757	6	AAD25729 Human cyc
2	654.4	26.9	2516	5	AAS69653 DNA encod
3	579	23.8	4380	13	ACN42631 Human dia
4	577.4	23.8	2607	8	ABZ80565 Nucleotid
5	573.6	23.6	3811	5	AAS91658 DNA encod
6	569.6	23.4	4238	10	ADB33355 Primary r
7	568	23.4	3236	13	ADB4556 Norway ra
8	518	21.3	2244	5	AAS76156 DNA encod
9	518	21.3	2244	5	AAS76184 DNA encod
10	223	9.2	3275	4	ABL19457 Drosophil
11	176.4	7.3	2500	10	ADD93243 Cyclic nu
12	176.4	7.3	2500	13	ADR24566 Breast ca
13	160.6	6.6	289	5	AAS75291 DNA encod
14	136.2	5.6	2109	4	ABL18085 Drosophil
15	133.2	5.5	3027	10	ADF56505 Modified
16	132.8	5.5	2615	12	ADQ67343 Novel hum
17	132.8	5.5	3486	10	AAD58492 Human CNG
18	131.6	5.4	1995	8	AAD56241 Rat CNG c
19	131.6	5.4	1995	8	AAD56239 Rat CNG c

20	131.6	5.4	1995	14	ADZ88276	Adz88276 Rat CNGA2
21	131.6	5.4	1995	14	ADZ88280	Adz88280 Mutated R
22	131.6	5.4	3027	10	ADF56506	Adf56506 Modified
23	131.6	5.4	3027	10	ADF56508	Adf56508 Rat olfac
24	129	5.3	526	4	ABA61898	Abas61898 Human foe
25	129	5.3	526	4	AAI41823	Aai41823 Probe #10
26	129	5.3	526	4	AAK36108	Aak36108 Human bon
27	129	5.3	526	4	AAK10209	Aak10209 Human bra
28	129	5.3	526	4	ABS35801	Abss35801 Human liv
29	128.4	5.3	1995	8	AAD56242	Aad56242 Rat CNG c
30	128.4	5.3	1995	8	AAD56240	Aad56240 Rat CNG c
31	128.4	5.3	1995	14	ADZ88282	Adz88282 Mutated R
32	128.4	5.3	1995	14	ADZ88278	Adz88278 Mutated R
33	128	5.3	2877	10	ADF56507	Adf56507 Modified
34	127	5.2	127	4	ABA74393	Aba74393 Human foe
35	127	5.2	127	4	AAI54858	Aai54858 Probe #23
36	127	5.2	127	4	AAK49030	Aak49030 Human bon
37	127	5.2	127	4	AAK22857	Aak22857 Human bra
38	127	5.2	127	4	ABS48687	Abss48687 Human liv
39	124.4	5.1	5133	4	ABU14931	Abu14931 Drosophil
40	120.6	5.0	5692	4	ABU19456	Abu19456 Drosophil
41	116.8	4.8	1989	8	ABX94804	Abx94804 Bovine CN
42	116.8	4.8	3166	13	ADS64555	Ads64555 Bovine cy
43	115.2	4.7	1989	8	ABX94805	Abx94805 Bovine CN
44	115.2	4.7	1992	13	ADS64558	Ads64558 Cyclic nu
45	113.6	4.7	1989	8	ABX94806	Abx94806 Bovine CN

ALIGNMENTS

RESULT 1
AAD25729
ID AAD25729 standard; DNA; 2757 BP.

XX AAD25729;

AC AAD25729;

DT 26-MAR-2002 (first entry)

XX Human cyclic nucleotide-gated cation channel 3 beta subunit DNA.

XX Human; cyclic nucleotide-gated cation channel 3 beta subunit; CNG3B;

KW cyclic nucleotide-gated ion channel; contraceptive; vision disorder;

KW male infertility; genetic defect; reporter-ligand interaction; CNG;

KW viral infection; cancer; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT misc_feature 1..49

FT /note= "These bases are absent in the sequence shown as

SEQ ID NO:2 in Page 64-65 of the specification"

FT CDS 112..2541

FT /tag= b

FT /product= "Human CNG3B protein"

FT /note= "This region is specifically claimed in claim 4 as

SEQ ID NO:4"

FT misc_feature 2753..2757

FT /tag= c

FT /note= "These bases are absent in the sequence shown as

SEQ ID NO:2 in Page 64-65 of the specification"

XX	PI	Creech CD, Jegla TJ;	Db		652	ACAGAACATTTACTACAGGCTGTGTGGTTCAAAGTCAAAAGATGCCTTTAACAGATAC	711
XX	DR	WPI; 2002-089847/12.	QY		601	TTAAGCGAATTAACATTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTTG	660
XX	DR	P-PSDB; AAE15982.	Db		712	TTAAAGCGAATTAACATTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTTG	771
XX	PT	New polypeptide, useful for screening for modulators of cyclic nucleotide	QY		661	TGCGCTCTTGCTGTGTCACCTCTTGCCTTATAACTGGAACCTGCTGGTTTATACCACTCGCCCTC	720
XX	PT	-gated ion channels, comprises the isolated cyclic nucleotide-gated	Db		772	TGCGCTCTTGCTGTGTCACCTCTTGCCTTATAACTGGAACCTGCTGGTTTATACCACTCGCCCTC	831
XX	PS	cation channel 3 beta subunit.	QY		721	GTCTTCCCATATCAAAACCGCAGACAACATACACTACTGCTTATTTGCGGACATCATATGT	780
XX	PS	Claim 4; Fig 2; 83pp; English.	Db		832	GTCTTCCCATATCAAAACCGCAGACAACATACACTACTGCTTATTTGCGGACATCATATGT	891
XX	CC	The invention relates to human cyclic nucleotide-gated cation channel 3	QY		781	GATATCATCTACCTTTATGATATGCTATTATCCAGCCAGACTCCAGTTTGTAAAGAGA	840
XX	CC	beta subunit (CNG3B) polypeptides and polynucleotides. CNG3B is a member	Db		892	GATATCATCTACCTTTATGATATGCTATTATCCAGCCAGACTCCAGTTTGTAAAGAGA	951
XX	CC	of cyclic nucleotide-gated cation channel (CNG) family. CNG3B forms	QY		841	GGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTT	900
XX	CC	functional heteromultimers with CNG1 and/or CNGA3, two CNG3 alpha	Db		952	GGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTT	1011
XX	CC	subunits that are expressed in retina. CNG3B polypeptides are useful for	QY		901	CAGTTGGATGTCGCATCAATAATACATTTGATATTTGCTACCTCTTCTTTGGGTTTAAAT	960
XX	CC	screening modulators of CNGs which are useful as contrareceptives and for	Db		1012	CAGTTGGATGTCGCATCAATAATACATTTGATATTTGCTACCTCTTCTTTGGGTTTAAAT	1071
XX	CC	treating various disorders involving cation channels, e.g. vision	QY		961	CCAAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCATCAC	1020
XX	CC	disorders and male infertility. Polynucleotides of the invention are	Db		1072	CCAAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAAATCATCAC	1111
XX	CC	useful for transfection of cells in vitro and in vivo, to correct	QY		1021	CTAGAGTCTATAAATGGACAAAGCATATATCTACAGAGTTATTCGAACAACTTCGATACATTG	1080
XX	CC	acquired and inherited genetic defects, cancer and viral infections.	Db		1132	CTAGAGTCTATAAATGGACAAAGCATATATCTACAGAGTTATTCGAACAACTTCGATACATTG	1191
XX	CC	Sequences of the invention are useful as reporter molecules in assays and	QY		1081	CTGTTTATTTGTCACATTAATGCTGTGTTTATTAATCTGGGCTTCAAACTATGAAGAAATTT	1140
XX	CC	detection systems, to measure changes in cation concentration, membrane	Db		1192	CTGTTTATTTGTCACATTAATGCTGTGTTTATTAATCTGGGCTTCAAACTATGAAGAAATTT	1251
XX	CC	potential, current flow, ion flux, transcription, signal transduction,	QY		1141	GGCACTACTAGATGGTGTATGATGGGGAAGAAACGAGTATCTGAGATGTTATTTATTTGG	1200
XX	CC	reporter-ligand interactions and second messenger concentrations, in	Db		1252	GGCACTACTAGATGGTGTATGATGGGGAAGAAACGAGTATCTGAGATGTTATTTATTTGG	1311
XX	CC	vitro, in vivo and ex vivo. They are useful to construct models of CNGs	QY		1201	GCAGTTCGAACTTTTAAATTAACCATTTGGTGGCTTCCAGAACCCACAACTTTATTTGAAATTT	1260
XX	CC	in a computer system and for examining expression and regulation of	Db		1312	GCAGTTCGAACTTTTAAATTAACCATTTGGTGGCTTCCAGAACCCACAACTTTATTTGAAATTT	1371
XX	CC	cation channels. The present sequence is a DNA encoding CNG3B protein	QY		1261	GTTTTTCAACTCTTGAATTTTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAAG	1320
XX	SQ	Sequence 2757 BP; 946 A; 571 C; 581 G; 659 T; 0 U; 0 Other;	Db		1372	GTTTTTCAACTCTTGAATTTTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAAG	1431
		Query Match 100.0%; Score 2430; DB 6; Length 2757;	QY		1321	ATGAGAGATGTGATTTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCTGCAATGGAT	1380
		Best Local Similarity 100.0%; Pred. No. 0;	Db		1432	ATGAGAGATGTGATTTGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCTGCAATGGAT	1491
		Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY		1381	GACACCATTTGCCCTACATGAAACAAATTAACCTTCCCTAAACTTGTGCAAAAGCGAGTTCGG	1440
QY	1	ATGTTTAAATCGCTGACAAAGTCAACAAAGTGAAGCCTATAGGAGAGAACAAATGAGAT	Db		1492	GACACCATTTGCCCTACATGAAACAAATTAACCTTCCCTAAACTTGTGCAAAAGCGAGTTCGG	1551
Db	112	ATGTTTAAATCGCTGACAAAGTCAACAAAGTGAAGCCTATAGGAGAGAACAAATGAGAT	QY		1441	ACTTGGTATGAATATACATGGGAGCTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAG	1500
QY	61	GAACAAGTTCCTGTCGGGAATGAAGAGGCTCTCACCCCAAGTAATCAGTCTCAGCAACC	Db		1552	ACTTGGTATGAATATACATGGGAGCTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAG	1611
Db	172	GAACAAGTTCCTGTCGGGAATGAAGAGGCTCTCACCCCAAGTAATCAGTCTCAGCAACC	QY		1501	ACCTTACCAACTACCGTCCAGTTAGCCCTCCGATTTGATGTAACCTTCCAGATCATCAGC	1560
QY	121	ACAGCACAGAGAGAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC	Db		1612	ACCTTACCAACTACCGTCCAGTTAGCCCTCCGATTTGATGTAACCTTCCAGATCATCAGC	1671
Db	232	ACAGCACAGAGAGAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC	QY		1561	AAAGTCGACTTGTTCAGAGGTTTGTATACAGAGATGATTTATGACATGTTGCTAAAGATTG	1620
QY	181	AGTCTGAAGAGCCACACCAACATACAAAGACAAATCTCTCCAAAGAAAATTCCTCTGGA	Db		1672	AAAGTCGACTTGTTCAGAGGTTTGTATACACAGATGATTTATGACATGTTGCTAAAGATTG	1731
Db	292	AGTCTGAAGAGCCACACCAACATACAAAGACAAATCTCTCCAAAGAAAATTCCTCTGGA	QY		1621	AAATCCGTTCTCTATTTGCCCTGGTGACTTTTCTGCCAAAAAGGAGAAATTTGGCAAGGAA	1680
QY	241	GATCTGACCAAAACCTGACCTCAAAATGAGAGAGAACCACTGGAACAGTGCAGAG					
Db	352	GATCTGACCAAAACCTGACCTCAAAATGAGAGAGAACCACTGGAACAGTGCAGAG					
QY	301	CAGAGGAAATGGACCCCGGGAAGAGAGTCCAAACAGCCCAACAAACAAACCGCTCGCA					
Db	412	CAGAGGAAATGGACCCCGGGAAGAGAGTCCAAACAGCCCAACAAACAAACCGCTCGCA					
QY	361	GCTCTGTTTAAATGAGTATGCCGATGCCAGCTACACAACTGTTGTAAGAAATGCGT					
Db	472	GCTCTGTTTAAATGAGTATGCCGATGCCAGCTACACAACTGTTGTAAGAAATGCGT					
QY	421	CAAGAACAGCCCTCTACAGAAATAAGTTGTTAGAGGAGATCTCTCCCTCACCCGAGCC					
Db	532	CAAGAACAGCCCTCTACAGAAATAAGTTGTTAGAGGAGATCTCTCTCCACCCGAGCC					
QY	481	AGCCCAACAACTGCAAGGCCACCGCTGTACCAACAGTAAAGAAAGCGATGATAGCCA					
Db	592	AGCCCAACAACTGCAAGGCCACCGCTGTACCAACAGTAAAGAAAGCGATGATAGCCA					
QY	541	ACAGAACATTACTACAGGCTGTTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGATAC					

1732	AAATCCGGTCTCTATTTGGCCCTGGTGACTTTTGCTCTGC AAAAAGGAGGAAATTTGGCAAGGAA	1791
1681	ATGTATATCATCAAGCATGGAGAAGTCCAAGTTCTTTGGAGGCCCTCATGTGACTAAAGTT	1740
1792	ATGTATATCATCAAGCATGGAGAAGTCCAAGTTCTTTGGAGGCCCTCATGTGACTAAAGTT	1851
1741	CTGGTTACTCTGAAAGCTGGGTCCGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGAGGA	1800
1852	CTGGTTACTCTGAAAGCTGGGTCCGGTGTTTGGAGAAATCAGCCTTCTAGCAGCAGAGGA	1911
1801	GGAAACCGTCCGAATCGTCAATGTGGTGGCCACGGGTTTGGCCAATCTTTTAACTCTAGAC	1860
1912	GGAAACCGTCCGAATGTGCTCAATGTGGTGGCCACGGGTTTGGCCAATCTTTTAACTCTAGAC	1971
1861	AAAAGACCCTCCAAAGAAATTTCTAGTGCATTATCCAGATTCTCAAGAGTCCCTCATGAAG	1920
1972	AAAAGACCCTCCAAAGAAATTTCTAGTGCATTATCCAGATTCTCAAGAGTCCCTCATGAAG	2031
1921	AAAGCCAGAGTGTCTTTTAAAGCAGAGAGGCTTAAGACCGCAGAACCCCTCCAAAGAAA	1980
2032	AAAGCCAGAGTGTCTTTTAAAGCAGAGAGGCTTAAGACCGCAGAACCCCTCCAAAGAAA	2091
1981	GATCTTTGCCCTCTCTTTCCACCGAAAGAGAGACACCCAAACTGTTTTAAACTCTCTCTA	2040
2092	GATCTTTGCCCTCTCTTTCCACCGAAAGAGAGACACCCAAACTGTTTTAAACTCTCTCTA	2151
2041	GGAGGCA CAGGAAAGCAAGTCTTTGCAGACTACTCAAATTTGAAGCGGAGAGCAAGCAGCT	2100
2152	GGAGGCA CAGGAAAGCAAGTCTTTGCAGACTACTCAAATTTGAAGCGGAGAGCAAGCAGCT	2211
2101	CAGAGAAAGAAATTTCTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2160
2212	CAGAGAAAGAAATTTCTGAAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	2271
2161	AAAGAAATCGAAGTAAACAAAGAAATTCAGATTAAGGAAAGGAAAGAGAGAGAGAGAGAG	2220
2272	AAAGAAATCGAAGTAAACAAAGAAATTCAGATTAAGGAAAGGAAAGAGAGAGAGAGAGAG	2331
2221	GATAAAGGAG	2280
2332	GATAAAGGAG	2391
2281	ATTGCAGTGGAGGAG	2340
2392	ATTGCAGTGGAGGAG	2451
2341	CGTCAATCACTCATTTATCAGCATGGCTCTTTCTGCTCAGGCGCGGAGAGAGAGTCTTTACT	2400
2452	CGTCAATCACTCATTTATCAGCATGGCTCTTTCTGCTCAGGCGCGGAGAGAGAGTCTTTACT	2511
2401	ATTGAAGTCAAGAAAGAGGCTTAAGCAATAA	2430
2512	ATTGAAGTCAAGAAAGAGGCTTAAGCAATAA	2541

RESULT 2

RECORDED 2
AAS69653
ID AAS69653 standard: CDNA: 2516 BP.

AA
AC AAS69653;

DT 13-FEB-2002 (first entry)

XX DE DNA encoding novel human diagnostic protein #5457.

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
 KW
 KW
 XX

XX Homo sapiens.

XX PN WO200175067-A2

XX
11-OCT-2001

30-MAR-2001; 2001WO-US008631.
31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
(HYSE-) HYSEQ INC.
Drmanac RT, Liu C, Tang YT;
WPI; 2001-639362/73.
P-PSDB; ABG05466.
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity.
Claim 1; SEQ ID NO 5457; 103pp; English.
The invention relates to isolated polynucleotide (I) and polypeptide (II)
sequences. (I) is useful as hybridisation probes, polymerase chain
reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
and in recombinant production of (II). The polynucleotides are also used
in diagnostics as expressed sequence tags for identifying expressed
genes. (I) is useful in gene therapy techniques to restore normal
activity of (II) or to treat disease states involving (II). (II) is
useful for generating antibodies against it, detecting or quantitating a
polypeptide in tissue, as molecular weight markers and as a food
supplement. (II) and its binding partners are useful in medical imaging
of sites expressing (II). (I) and (II) are useful for treating disorders
involving aberrant protein expression or biological activity. The
polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependant on DNA and
amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
coding sequences of the invention. Note: The sequence data for this
patent did not appear in the printed specification, but was obtained in
electronic format directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences

Query Match 26.9%; Score 654.4; DB 5; Length 2516;
Best Local Similarity 99.1%; Pred. No. 1.5e-133;
Matches 658: Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy	1767	GTTTGGAGAAATCAGCCTTCTAGCAGCAGAGGAGGAAACCGTCGAACTCGCCAAATGTGGT	1826
Db	1853	GTCAAGAAAACAACAGCCTTCTAGCAGCAGGAGGAGGAAACCGTCGAACTCGCCAAATGTGGT	1912
Qy	1827	GGCCACGGGTTTGGCCAAATCTTTTAACTCTAGACAAAGAGACCCCTCCAAGAAATTTCTAGT	1886
Db	1913	GGCCACCGGGTTTGGCCAAATCTTTTAACTCTAGACAAAGAGACCCCTCCAAGAAATTTCTAGT	1972
Qy	1887	GCATTATCCAGATTCTGAAAGGATCCCTCATGAAGAACCCAGAGTGCTTTTAAAGCAGAA	1946
Db	1973	GCATTATCCAGATTCTGAAAGGATCCCTCATGAAGAACCCAGAGTGCTTTTAAAGCAGAA	2032
Qy	1947	GGCTAAGACCGCAGAGCAACCCCTCCAAGAAAGATCTTGGCCCTCTCTTCCCACCCGAA	2006
Db	2033	GGCTAAGACCGCAGAGCAACCCCTCCAAGAAAGATCTTGGCCCTCTCTTCCCACCCGAA	2092
Qy	2007	AGAAAGACACCCAAAATGTTTTAAAACTCTCTAGGAGGCACAGGAAAAAGCAAGTCTTGC	2066
Db	2093	AGAAAGACACCCAAAATGTTTTAAAACTCTCTAGGAGGCACAGGAAAAAGCAAGTCTTGC	2152
Qy	2067	AAGACTACTCAAAATGAAGCGCAGAGCAAGCAGCTTCAGAACGAGAAATTTCTGAAGGAGG	2126
Db	2153	AAGACTACTCAAAATGAAGCGCAGAGCAAGCAGCTTCAGAACGAGAAATTTCTGAAGGAGG	2212
Qy	2127	AGAGAGAGAGGAAAGAGAAATGAAGATTAACAAAAAGAAATTCGAGATTAACAAAAAGA	2186

Db 2765 TGAATTTCTACAGATCCCAAGTCGTCGAGAACCGCGTCAAGACCTGGTAGGATACA 2824
 QY 1457 CATGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAGACCCCTACCAACTACGG 1516
 Db 2825 CCTGGCACTCGCAAGCATGCTGGATGAGTCAGAGCTGATGGTGCAGCTTCCAGACAAGA 2884
 QY 1517 TCCAGTAGCCCTCGCCATGATGTGAACCTTCAGCATCATCAGCAAGTCGACTTGTTC 1576
 Db 2885 TCGGCTGGACCTCGCCATCGAGCTGAACCTTACAACATCGTTAGCAAGTCGCACTCTTTC 2944
 QY 1577 AGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCGGTTCTCTATT 1636
 Db 2945 AGGGCTGTGACCGGAGATGATCTTTGACATGCTGAAGGCTTCGCTCTGTGTCTACC 3004
 QY 1637 TGCCTGGTGACTTGTCTGCAAAAAGGGAGAAATTCGCAAGGAAATGTATATCATCAAG 1696
 Db 3005 TGCCCAACGACTATGTGTGCAAGAAGGGGAGATCGGCCGTGAGATGTATCATCATCCAG 3064
 QY 1697 ATGGAGAAGTCCAAGTCTTGGAGGCCCTGATGCTACTAAAGTTCTGTTACTCTGAAG 1756
 Db 3065 CAGGGCAAGTCGAGGTCTTGGCGGCCCTGATGGGAAATCTGTGCTGGTGACGCTGAAG 3124
 QY 1757 CTGGCTCGGTTTGGAGAAATCAGCTCTTAGCAGCAGGAGGAGAAACCGTCGAACTG 1816
 Db 3125 CTGANTCTGTGTTGGAGAAATTAAGCTTGTCTGCTGTGGGGCGGGAAACCGGCGCAGG 3184
 QY 1817 CCAATGTGTGGCCACGCGGTTTGCCTAATCTTTTAACTCTAGACAAAAGACCTCCAAG 1876
 Db 3185 CCAACGTGTGGCCACGCGGTTTACCAACCTCTTATCTCTGGATAAGAAGGACCTGAATG 3244
 QY 1877 AAATCTAGTGATATTCAGATTCGAAAGGATCTCATGAAAGAACCCAGAGTGTCTTT 1936
 Db 3245 AGATTTTGTGTGATATCTCTGAGTCTCAGAAATTACTCCGGAAGAAAGCCAGCGCATGC 3304
 QY 1937 TAAGCAGAGGCTTAAGACCGCAGAG 1963
 Db 3305 TGAAAGCAACAATAAGCCCAAGAGG 3331

RESULT 4

ID ABZ80565 standard; cDNA; 2607 BP.

XX AC ABZ80565;

XX 26-JUN-2003 (first entry)

XX Nucleotide sequence of hbeta1b.

XX OCN1; OCN2; beta1b; CNG; human;
 KW olfactory cyclic nucleotide gated channel subunit; ss.

XX Homo sapiens.

XX W02003004611-A2.

XX 16-JAN-2003.

XX 08-JUL-2002; 2002MO-US021184.

XX 06-JUL-2001; 2001US-0303140P.

XX 10-DEC-2001; 2001US-0337154P.

XX (SENO-) SENOMYX INC.

XX Zoller MT, Xu H, Staszewski L, Moyer B, Pronin A, Adler JB;

PI Servant G, Callamaras N;

XX WPI; 2003-229406/22.

XX P-PSDB; ABR39396.

XX Novel isolated nucleotide sequences encoding human OCN1, OCN2, beta 1b
 PT olfactory cyclic nucleotide gated (CNG) channel subunits, useful for

PT identifying the CNG channel activators useful for enhancing smell.
 XX Claim 14; Page 89; 97pp; English.
 PS The present invention relates to a nucleotide sequences encoding human
 CC OCN1, OCN2, or beta1b olfactory cyclic nucleotide gated (CNG) channel
 CC subunit, its action being an olfactory CNG channel activity modulator. A
 CC host cell which expresses human OCN1, OCN2 and/or beta1b is useful in a
 CC mammalian cell-based assay for the profiling and screening of putative
 CC modulators of a human olfactory cyclic nucleotide gated (CNG) channel.
 CC The method is used to identify a compound as one which particularly
 CC modulates CNG activity based on a detectable change in fluorescence. The
 CC test cell expresses each of the human OCN1, human OCN2 and human beta1b
 CC subunits. A fluorescence plate reader or a voltage imaging plate are used
 CC to monitor changes in fluorescence. The compounds that activate olfactory
 CC CNG channel enhance smell and can be used to make foods more palatable
 CC for individuals with attenuated olfactory function. The present sequence
 CC represents the nucleotide sequence of hOCN1
 XX Sequence 2607 BP; 614 A; 782 C; 719 G; 492 T; 0 U; 0 Other;
 SQ

Query Match 23.8%; Score 577.4; DB 8; Length 2607;

Best Local Similarity 64.3%; Pred. No. 1.2e-116;

Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY 617 TTCCAAACAGCATAGATTTCATACAGATCGACTCTATCTCTGTGGCTCTTCTGTCTCA 676
 Db 782 TTCCCAAGAGCATGACCGCTGACCAACCTGATGTATGCTTATGGCTGTCTTCTGTGG 841
 QY 677 CTCCTCCCTATTAACCTGAACTGCTGTTTATACACTGGCGCTCTTCCCATATCAAA 736
 Db 842 TGATGCCCTGGAAATGGAACTGTTGGCTGATTCCTGTGGCTGGCGCTTCCCTACAGA 901
 QY 737 CCGCAGACAACATACACTACTGGCTTATTTCCGGACATCATATGTATATCATCTACTCT 796
 Db 902 CCCCAGACAACATCCACACTGGCTGCTGATGATTTACCTATCGACCTCATCTACTTCC 961
 QY 797 ATGATATGCTATTTATTCAGCCCGAGACTCCAGTTTGTAGAGAGGAGAGACATAAGTGG 856
 Db 962 TGGACATACCGTGTTCAGACACGCTGCAGTTTGTGAGAGCGGGGACATCATTAACGG 1021
 QY 857 ATTCAAAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTTTCAGTTCCGATGCCAT 916
 Db 1022 ACAAAGGACATGCGAAATAACTACTGAACTCTCGCCGCTTCAAGATGGAGCTGCTCA 1081
 QY 917 CAATAATACCATTTGATATTTTGTACCTCTTCTTGGGTTTAAATCCAAATGTTTACGCAA 976
 Db 1082 GCCTCCTGCCCTTGGATTTTCTCTATTTGAAAGTCGGTGTGAACCCCTCTCCGCCCTGC 1141
 QY 977 ATAGGATGTTAAAGTACACTTCAATTTTGAATTTTAATCATCAGCTAGAGTCTATAATGG 1036
 Db 1142 CCGCTGTTTAAAGTACATGGCCCTTCTTCGAGTTTAAACAGCCGCTGGAAATCCATCTCA 1201
 QY 1037 ACAAGCATATATCTACAGAGTTTATTCGAACAACCTGATACTTGTCTTTATTCCTGCACA 1096
 Db 1202 GCAAAGCTACGTGTACAGGGTCATCAGGACCAAGCCTACCTTCTCTACAGCCTGCAAT 1261
 QY 1097 TTAATGCCTGTGTTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGG 1156
 Db 1262 TGAATTCCTGTCTTTTACTGGGCTATCGGCTATCAGGCGCTCGGCTCCACTCAGTGG 1321
 QY 1157 TGTATGATGGGGAAGGAACGAGTATCTGAGATGTTTATTTATTTGGGAGTTCGAACTTAA 1216
 Db 1322 TTTACGATGGCGTGGGAAACAGTTATATTCGCTGTTACTACTTGTGTGTAAGACCCCTCA 1381
 QY 1217 TTACCATTTGGGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCACACTCTGA 1276
 Db 1382 TCACCATCGGGGCTGCTTGACCCCAAGACACTCTTTTGAATTTGTTTCCAGCTGCTGA 1441
 QY 1277 ATTTTCTTCTGGAGTTTGTGTTCTTCCAGTTTAAATTTGGTCAGATGAGATGTGATTG 1336
 Db 1442 ATTATTTACGGGCTCTTGTCTTCTCTGTGATGATCGGACAGATGAGATGTGATTG 1501

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QY 1337 GAGCAGCTACAGCAATCAGAACTACTTCGGCGCCTGCGATGATGATGACACCACTTGCCCTACA 1396
D 1502 GGGCCGCCACCGGGGACAGACCTACTACCGCAGCTGCTGACAGCAGCGGTGAAGTACA 1561
QY 1397 TGAACAATTACTCCATTCTCTAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATA 1456
D 1562 TGAATTTCTAAGATCCCAAGTCGCTGCAGAACCGCGTCAAGACTTGGTACGAGTACA 1621
QY 1457 CATGGACTCTCAAGAATCTAGATGAGTCTGATTTGGCTTAAGACCCCTACCAACTACCG 1516
D 1622 CTTGGCACTCGCAAGCATGCTGGATGAGTCAGAGCTGATGCTGCAGCTTCAGACAAGA 1681
QY 1517 TCCAGTTAGCCCTCGCCATGTGTAATCTTGAATCATACAGCAAGTTCGATCTGTTTCA 1576
D 1682 TCGCGCTGACCTCGCCATCGAGCTGAACTCAACAATCGTTAGCAAAAGTCGCACCTTTTC 1741
QY 1577 AGGGTGTGCATACACAGATGATTTATGACATGTTGCTTAAGATGAAATCGTCTCTATT 1636
D 1742 AGGGCTGTACCGGAGATGATCTTTGACATGCTGAAGAGGCTTCGCTCTGTTGCTACC 1801
QY 1637 TGCCTGGTGAATTTGTCTCAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC 1696
D 1802 TGCCCAACGACTATGTGCAAGAGGGGAGATCGGCCGTGAGATGTATCATCATCCAGG 1861
QY 1697 ATGGAGAAGTCAAGTCTTTGGAGGCCCTGATGGTACTAAAGTTCGTGTTACTCTGAAG 1756
D 1862 CAGGGCAAGTGCAGGCTTTGGGCGGCCCTGATGGGAAATCTGTCTGTTGACGCTGAAG 1921
QY 1757 CTGGGTGCGTGTGGAGAAATCAGCTTCTAGCAGGAGGAGAAACCGTCGAACTG 1816
D 1922 CTGGATCTGTGTTGGAGAAATGAAGTCTGTGCTGTGGGCGGGAACCGGCGACGG 1981
QY 1817 CCAATGTGTGGCCCAACGGGTTTGCAATCTTTTAACTCTAGACAAAAGACCTCCAAAG 1876
D 1982 CCAAGCTGTGGGCACGCGGTTTACCAACTCTTCATCTGTGATAAGAGGACCTGAATG 2041
QY 1877 AAATCTAGTGATATCCAGATCTGAAAGGATCTCATGAAAGACCGCAAGCGAGTGCTTT 1936
D 2042 AGATTTGTGTGATATCTCTGAGTCTCAGAAGTTACTCGGAAGAAAGCGGCGCATGC 2101
QY 1937 TAAAGCAGAAGCTTAAGACCGCAGAG 1963
D 2102 TGAAGACCAATTAAGCCCAAGGAGG 2128

RESULT 5
ID AAS91658
XX AAS91658 standard; cDNA; 3811 BP.
AC AAS91658;
XX
XX 13-FEB-2002 (first entry)
XX
XX DNA encoding novel human diagnostic protein #27462.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
XX 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
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DR WPI; 2001-639362/73.
DR P-PSDB; ABG27471.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 27462; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (II) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (I) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 3811 BP; 812 A; 1093 C; 1102 G; 804 T; 0 U; 0 Other;
```

```
Query Match 23.6%; Score 573.6; DB 5; Length 3811;
Best Local Similarity 64.6%; Pred. No. 9.6e-116;
Matches 855; Conservative 0; Mismatches 469; Indels 0; Gaps 0;
QY 640 ACAGACTCGACTCTATCTCTCTGGCTCTTGCTTGTCACCTCTTGCCCTATAACTGGAACCTGC 699
D 2009 ACAGACCTGATGATGCTATGCTGCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2068
QY 700 TGGTTTATACCACCTGCGCTCTCTTCCCATATCAACCCGAGACCAACATACACTACTGG 759
D 2069 TGGCTGATTCCTGCTGCGCTTCCCTTACCAGACCCCGGACCAACATCACCACTGC 2128
QY 760 CTTATTGCGGACATCATATGATGATCATCTACCTTTTATGATGCTATTATTCAGTCC 819
D 2129 CTGCTGATGGATTACCTATGCGACCTCATCTACTTCTCTGGACATCACCGTGTTCAGACA 2144
QY 820 AGACTCCAGTTTGTAAAGAGGAGAGACATAATAGTGGATTCAATAGACTAAGGAACAC 874
D 2189 CGCTGCGAGTTTGTGAGAGCGGGGACATCATATCGGACAAAAGGACATCGAATAATAC 2248
QY 880 TACAGGACTTCTACAAAATTTTCAGTTGGATGCGCATCAATAATACCAATTTGATATTTGC 939
D 2249 TACCTGAAGTCTCGCGGCTTCAAGATGAGACCTGCTCAGCCTCTGCTGCTGCTGCTGCT 2308
QY 940 TACCTCTCTTTGGGTTTAAATCCAAATGTTTGAAGCAATAGATGTTTAAAGTACACTTCA 999
D 2309 TATTGAAAGTCGGTGTGAACCCCTCTCTCGCCCTGCCCCCTGTTTAAAGTACATGCCC 2368
QY 1000 TTTTGTGAATTTAATCATCATCTAGAGTCTAATAATGGACAAAGCATATATCTACAGAGTT 1059
D 2369 TTCTTCGAGTTTAAAGCGGCTGGAATCCATCTCAGCAAAAGGCTACGTGTACAGGGTTC 2428
QY 1060 ATTCGAACAACCTGGATCTTGTGTTTATCTCGACATTAATAGCTGTGTTTATTACTGG 1119
D 2429 ATCAGGACCACAGCCTACCTTCTCTACAGCCTGCAATTTGAATTCCTGCTTCTTATTACTGG 2488
QY 1120 GCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGGTGATGATGGGGAAGGAACAG 1179
D 2489 GCATCGGCCCTATCAGGGCCTCGGCTCCACTCACTGGGTTTACGATGGCGTGGGAACAGT 2548
```


QY 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGAGACATAATAGTGG 856
|||
Db 2457 TGGACATCACCGTGTCCAGATCGCTCCAGTTTGTCAAAGCGCGGACATCATACAG 2516
|||
QY 857 ATTCAAATGAGCTAAGGAACACTACAGACTTCTACAAATTTTCAGTTGGATGTCGAT 916
|||
Db 2517 ATAAGAGGAGATGCGTAATAATTACTGAAGTCTCAACGATTTAAGATGGACTTGTCT 2576
|||
QY 917 CAATAATACCATTTGATATTTGCTACTCTCTTTTGGGTTTAAATCAATGTTTATAGACAA 976
|||
Db 2577 GCCTTTGCTTTGGATTTCTCTACTTGAACCTTGGCGTGAACCCCTTCTTGGCTGC 2636
|||
QY 977 ATAGGATGTAAGTACACTTCATTTTGAATTTAATCATCACCTAGAGTCTATATGG 1036
|||
Db 2637 CCGCTGCGCTGAAGTACATGGCTTCTTTGAGTTTAATAACCGTCTGGAAGCCATCCTCA 2696
|||
QY 1037 ACAAGCATATATCTACAGAGTTATTGGAACAACTGATACCTTGTGTTTATTTCGCACA 1096
|||
Db 2697 GCAAGCCTACGTTTACAGGTTTATCAGGACCAACCCCTACTCTGTATAGCTTGCATC 2756
|||
QY 1097 TTAATGCTGTGTTTATTACTGGGCTTCAAACTATGAAGAAATTGGCACTACTAGATGG 1156
|||
Db 2757 TCAACTCTGTCTTTACTACTGGCGTGGCCCTTCCAGGGCATCGTTCCACTCACTGGG 2816
|||
QY 1157 TGTATGATGGGAAGGAACGAGTACTGAGATGTTATTTATTTGGGAGTTCGAACTTTAA 1216
|||
Db 2817 TTTATGACGGCTGGGGAACAGCTACTTCGATGCTACTACTGGCTGTGAAAACCTCTCA 2876
|||
QY 1217 TTACCAATCGTGGCTTCCAGAACCAAACTTTATTGAAATGTTTTCACCTCTTCA 1276
|||
Db 2877 TCACCAATCGAGACTGCCCGACCCAGACGCTCTTTGAGATCGTCTTCCAGCTGCTGA 2936
|||
QY 1277 ATTTTCTGAGTCTTTGTTGTTCTCCAGTTTAAATGGTCAGATGAGAGATGTGATG 1336
|||
Db 2937 ATTTTACAGGTGCTTCGCTTCTCTGTGATGATTGGACAGATGAGAGATGGTGG 2996
|||
QY 1337 GAGCAGTACAGCAATCAGAACTACTTCGGCGCTGATGATGATGACACCATTCGCTCA 1396
|||
Db 2997 GGGCGCCACGGCGGAGAGAGCTACTACCGAGCTGCATGGACAGCAGCGTGAAGTACA 3056
|||
QY 1397 TGAACAATTAATCTCATTTCTTAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATA 1456
|||
Db 3057 TGAATCTTACAGATCCCCAGGTCTGTGAGAACCCGCTCAAGACTGGTAGAATA 3116
|||
QY 1457 CATGGACTCTCAAAGAACTAGATGAGTCTGATTTGCTTAAGACCCCTACCAACTACGG 1516
|||
Db 3117 CTTGGCACTCACAAGCATGCTGGATGAGTCAAGCTGATGTTCACTTCCGGAACA 3176
|||
QY 1517 TCCAGTTAGCCCTCGCATTTGATGAACTTCAGCATCATCAGCAAGTTCGACTTGTTC 1576
|||
Db 3177 TCGCTCTGACCTGGCCATTTGACGTAACTACAACTTGTCAAGAAAGTGGCGCTCTCC 3236
|||
QY 1577 AGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTTGAATCCGTTCTCTATT 1636
|||
Db 3237 AGGCTGCGACCGGAGATGATCTTCAGCATGCTCAAGCATCTCGCTCAGTCTCTACC 3296
|||
QY 1637 TGCCTGGTGACTTTGTCTCAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGC 1696
|||
Db 3297 TACCCAATGACTATGTGTCAAGAGAGGGGAGATTGGCCGAGAGATGTATATTATCCAG 3356
|||
QY 1697 ATGGAGAACTCCAAGTTCTTGGAGGCCCTGTAGTGTACTTAAAGTTCTGGTTACTCTGA 1756
|||
Db 3357 CGGGGAGGTGAGGTGCTGGGCGGCCAGATGGAAGAGGCTGTCTCTGGTGACACTCAAG 3416
|||
QY 1757 CTGGGTGCGTGTGAGAAATCAGCCTTCTAGCAGCAGGAGGAGAAACCGTCAAGCTG 1816
|||
Db 3417 CCGGATCGGTGTTGGAGAGATAAGTCTGTGCTGTCTGGGGCGGTATACGGCGCACGG 3476
|||
QY 1817 CCAATGTGTGCCCCACGGGTTTGGCAATCTTTTAACTCTAGACAAAAGACCCCTCCAA 1876
|||
Db 3477 CCAATGTGTGCCCCACGGCTTCAACCAATCTCTTCAATCTCGGATAGAAGGACTTGAATG 3536
|||
QY 1877 AAATCTAGTGCAATATCCAGATTTCTGAAGAGATCTCTCATGAAGAACCCAG 1928
|||

Db 3537 AGATTTTGGTCATTTACCTGAATCTCAGAAGCTGCTCCGGAAGAGCCAG 3588
|||

RESULT 7

AD564556
ID ADS64556 standard; DNA; 3236 BP.

XX ADS64556;

XX 16-DEC-2004 (first entry)

XX Norway rat cyclic nucleotide-gated ion channel 4.3 (CNG4.3) DNA.

XX cyclic nucleotide concentration; screening;

XX cyclic nucleotide-gated ion channel 4.3; CNG4.3; db.

XX Rattus norvegicus.

XX WO2004083803-A2.

XX 30-SEP-2004.

XX 06-MAR-2004; 2004WO-EP002317.

XX 18-MAR-2003; 2003DE-01011769.

XX (FARB) BAYER HEALTHCARE AG.

XX Wunder F;

XX WPI; 2004-728498/71.

Determining intracellular concentration of cyclic nucleotides, useful for identifying, e.g. receptor ligands and enzyme inhibitors, comprises using cells that express a cyclic nucleotide activated ion channel and a photoprotein.

Example; SEQ ID NO 2; 20pp; German.

The invention relates to a novel method for determining the intracellular concentration of cyclic nucleotides. The method comprises preparing a cell that expresses a CNG (cyclic nucleotide-activated) ion channel together with a photoprotein and detecting the intracellular concentration of cyclic nucleotides from the luminescent signal of the photoprotein. The method may be used to screen for receptor ligands and modulators of phosphodiesterase, guanylate cyclase or nitric oxide synthase, which would be potentially useful as pharmaceuticals. The method is suitable for high throughput screening, does not require radioactive tracers, has a high signal-to-noise ratio, is very quick, highly sensitive and inexpensive. The current sequence is that of the Norway rat cyclic nucleotide-gated ion channel 4.3 (CNG4.3) DNA of the invention.

Sequence 3236 BP; 780 A; 962 C; 903 G; 591 T; 0 U; 0 Other;

Query Match 23.4%; Score 568; DB 13; Length 3236;
Best Local Similarity 64.6%; Pred. No. 1.5e-114;
Matches 847; Conservative 0; Mismatches 465; Indels 0; Gaps 0;

QY 617 TTCAAAACAGCATAGATTCATACACAGATCGACTCTATCTCTGTGGCTTCTTGTCTCA 676
|||

Db 1211 TCCCCCAGAGCATCGCCCACTGACCAACCTCATGTACATCTCTGTGGCTGTCTGTGG 1270
|||

QY 677 CTCTTGGCTTAACTGGAAGTCTGGTTTATACCACTCGGCTCTTCCCATATCAAA 736
|||

Db 1271 TCTGGCTGGAATGGAAGTCTGCTGATTTCTGTGGCTGGGCCCTTCCCGTACCAGC 1330
|||

QY 737 CGGCAGACAACATACACTACTGGCTTTATGGGGACATCATATGTATCATCTACCTTT 796
|||

Db 1331 GGGCAGACAACATCCACCTCTGGCTGCTCATGGACTACTTGTGGCACTTCATCTACC 1390
|||

QY 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTGAAGAGGAGGAGACATAATAG 856
|||


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Db 1391 TGGACATCACCGTGTTCAGATCGCTCCAGTTTGTCAAGCGGGGACATCATTTACAG 1450
Qy 857 ATTCAATGAGCTAAGGAAACACTACAGGACTTCTACAAATTTAGTTGGATGCGCAT 916
Db 1451 ATAAGAGGAGATGCGTAATTAATTAAGTCTCAACGATTTAAGATGGACTTGCTCT 1510
Qy 917 CAATAATACCAATTTGATATTTGTTACTCTCTTTGGGTTTAATCAATGTTTGAAGCAA 976
Db 1511 GCCTTTTGGCTTTGATTTCTCTACTTGAACCTGGCGTGAACCCCTCTTTCGCGCTGC 1570
Qy 977 ATAGGATGTTAAGTACACTTCAATTTTGAATTTAATCATCACTAGAGTCTATAATGG 1036
Db 1571 CCGCTGCTGAAATGATCATGGCTTCTTTGAGTTTAATAACGCTGGAAGCCATCCTCA 1630
Qy 1037 ACAAGCATATATCTACAGAGTTATTGGAACAACTGATACTTGTCTTTATTCTGCACA 1096
Db 1631 GCAAGCTACGTTTACAGGTTTATCAGGACCAACCGCTACCTGCTGTATAGCTTGATC 1690
Qy 1097 TTAATGCTGTGTTTATTACTGGGCTTCAAACCTATGAAGGAATTTGGCACTACTAGATGG 1156
Db 1691 TCAACTCTCTCTTACTACTGGGCTGGCCCTTCCAGGGCATCGGTTCCACTCACTGGG 1750
Qy 1157 TGTATGATGGGAAGGAAACGATATCTGAGATGTTATTATTTGGGCACTTCGAACCTTAA 1216
Db 1751 TTTATGACGGCGTGGGAAACAGCTACATTCGATGCTACTACTGGGCTGTGAAAACCTCA 1810
Qy 1217 TTACCATTTGTGGCTTCCAGAACCAACAACTTTATTGAAATTTGTTTCAACTCTTGA 1276
Db 1811 TCACCATCGGAGACTGCCGACCCCGACGCTCTTTGAGATGCTCTTCAGTGTCTGA 1870
Qy 1277 ATTTTCTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGTGANTG 1336
Db 1871 ATTATTTTACAGGTGCTCTCGCTTCTCTGTGATGATTTGACAGATGAGAGATGTGTTG 1930
Qy 1337 GAGCAGCTACAGCAATCAGAACTAATTCGCGGCTGCTGATGATGATGACACCATTCGCTACA 1396
Db 1931 GGGCCGCGCAGCGGAGGACAGCTACTACCGGACGCTGCATGGACAGCAGCGTGAAGTACA 1990
Qy 1397 TGAACAAATTAATCTCAATCTTAACTTGTGCAAAAGCGAGTTCCGACTTGTGTATGAATATA 1456
Db 1991 TGAATCTTCAAGATCCCGAGGTCTGTGCAAGAACCCGCTCAAGACCTGTTATGATGATACA 2050
Qy 1457 CATGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAAGACCCCTACCAACTACGG 1516
Db 2051 CTTGGCAATTCACAGGCACTGCTGATGAGTCAGAGCTGATGTTTTCAGCTTCCGGACAAGA 2110
Qy 1517 TCCAGTTAGCCCTCGCCATTTGATGTGAATTCAGCATCATCAGCAAGTGCATTTGTCA 1576
Db 2111 TGGCTCTGGACCTGGCCATTTGACGTAAACTACAACATTTGTGACCAAAAGTGGCGCTCTCC 2170
Qy 1577 AGGCTGTGTATACACAGATGATTTATGACATGTTTGTGCTAAAGATTGAAATCGCTTCTATT 1636
Db 2171 AGGCTGTGTATACACAGATGATTTATGACATGTTTGTGCTAAAGATTGAAATCGCTTCTATT 1636
Qy 1637 TGCCTGTGTGATTTTGTCTGCAAAAAGGAGAAATTTGGCAAGAAATGATATATCATCAAGC 1696
Db 2231 TACCAATGACTATGTGTGCAAGAGGGGAGATTTGGCCGAGAGATGTATATTTATCCAGG 2290
Qy 1697 ATGAGAGATCCAAATTTCTTGGAGCCCTGATGTGATCAATGTTCTGTTACTCTGAAAG 1756
Db 2291 CGGGCGAGGTGCAGTGTGTGGCGGCCGACATGAAAGGCTGTCTGTGTGACACTCAAG 2350
Qy 1757 CTGGGTGCTGTTTGGAGAAATCAGCTTCTAGCAGCAGGAGGAGAACCGTTCGAATCTG 1816
Db 2351 CCGATCGGTGTTTGGAGAGATAAGCTTGTGCTGTCTGGGGGGGTAACAGGCGCAGG 2410
Qy 1817 CCAATGTGTGGCCCAACGGGTTTGCAATCTTTTAACTCTAGACAAAAGACCTCTCCAAG 1876
Db 2411 CCAATGTGTGGCCCAACGGGTTTGCAATCTTTTAACTCTAGACAAAAGACCTCTCCAAG 1876
Qy 1877 AAATTTAGTGCATTTATCCAGATTTCTGAAAGGATTCCTCATGAAGAGCCAG 1928
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Db 2471 AGATTTTGTGTCATTACCTGTAATCTCAGAGCTGCTCCGGAAGAAGCCAG 2522
RESULT 8
AAS76156
ID AAS76156 standard; cDNA; 2244 BP.
XX AAS76156;
AC AAS76156;
XX 13-FEB-2002 (first entry)
DT DNA encoding novel human diagnostic protein #11960.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US008631.
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
PI WPI; 2001-639362/73.
DR P-PSDB; ABG11969.
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX Claim 1; SEQ ID NO 11960; 103pp; English.
PS The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC parent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2244 BP; 720 A; 469 C; 592 G; 463 T; 0 U; 0 Other;
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Query Match 21.3%; Score 518; DB 5; Length 2244;
Best Local Similarity 94.7%; Pred. No. 1.3e-103;
Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
Qy 287 GAACAGTGCAGAGCAGAGAAATGGACCCCGGAAAGAGGTCCCAACAGCCCAAAA 346
Db 83 GCMAACTATCACAGGACAGAAACCAACACCCGATGTTCTTCACACAGCCCAAAA 142
```

QY 347 ACAAAACCGCTCGAGCTCTCTGTATATAAATGAGTATGCCGATGCCAGCTACACAACCTGG 406
Dd |||||
QY 143 ACAAAACCGCTCGAGCTCTCTGTATATAAATGAGTATGCCGATGCCAGCTACACAACCTGG 202
Dd |||||
QY 407 TGAAGAAGTATGGTCAAGAACAGCCCTCTACAAAGAAAAGTTGGTAGAGGAGATCTCT 466
Dd |||||
QY 203 TGAAGAAGTATGGTCAAGAACAGCCCTCTACAAAGAAAAGTTGGTAGAGGAGATCTCT 262
Dd |||||
QY 467 CCTCACCCGAAGCCAGCCACAAACTGCAAAAGCCACAGCGCTGTACCCACAGTAAAGAAA 526
Dd |||||
QY 263 CCTCACCCGAAGCCAGCCACAAACTGCAAAAGCCACAGCGCTGTACCCACAGTAAAGAAA 322
QY 527 GCGATGATAAGCAACAGAACATTACTACAGGCTGTGGTTCAAAGTCAAAAGATCC 586
Dd |||||
QY 323 GCGATGATAAGCAACAGAACATTACTACAGGCTGTGGTTCAAAGTCAAAAGATCC 382
QY 587 CTTTAAACAGTACTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACACAGATC 646
Dd |||||
QY 383 CTTTAAACAGTACTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACACAGATC 442
QY 647 GACTCTATCTCCTGTGGCTCTTGTCTGTGTCACCTCTTGCCTATTAAGTGAAGTCTGTGTTTA 706
Dd |||||
QY 443 GACTCTATCTCCTGTGGCTCTTGTCTGTGTCACCTCTTGCCTATTAAGTGAAGTCTGTGTTTA 502
QY 707 TACCACCTGCGCTCTGCTCTTCCCATATCAAAACCGCAGACAAACATACACTACTGGCTTATTG 766
Dd |||||
QY 503 TACCACCTGCGCTCTGCTCTTCCCATATCAAAACCGCAGACAAACATACACTACTGGCTTATTG 562
QY 767 CGGACATCATATGTGATATCATCTACCTTATGATATGCTATTATCCAGGCCAGACTCC 826
Dd |||||
QY 563 CGGACATCATATGTGATATCATCTACCTTATGATATGCTATTATTCAGGCCAGACTCC 622
QY 827 AGTTTGTAAAGAGGAGGAGACATAATA 852
Dd |||||
QY 623 AGTTTGTAAAGAGGAGGAGACATAATA 648

RESULT 9

AA576184/c
ID AA576184 standard; cDNA; 2244 BP.
XX
AC AA576184;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #11988.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG11997.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
XX biodiversity.

PS Claim 1; SEQ ID NO 11988; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AA564197-AA594564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2244 BP; 463 A; 592 C; 469 G; 720 T; 0 U; 0 Other;
Query Match 21.3%; Score 518; DB 5; Length 2244;
Best Local Similarity 94.7%; Pred. No. 1.3e-103;
Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 287 GAACAGTCCGAGAGAGAGAAATGGACCCCGGAAAGAGGTCCAAACAGCTCCACAA 146
Dd |||||
QY 2162 GCAAACTATCAAGGACAGAAAACCAACACCGCATGTTCTCACACAAACGCCACAA 2103
QY 347 ACAAAACCGCTCGAGCTCTCTGTATATAAATGAGTATGCCGATGCCAGCTACACAACCTGG 406
Dd |||||
QY 2102 ACAAAACCGCTCGAGCTCTCTGTATATAAATGAGTATGCCGATGCCAGCTACACAACCTGG; 2043
QY 407 TGAAGAAGTATGGTCAAGAACAGCCCTCTACAAAGAAAAGTTGGTAGAGGAGATCTCT 466
Dd |||||
QY 2042 TGAAGAAGTATGGTCAAGAACAGCCCTCTACAAAGAAAAGTTGGTAGAGGAGATCTCT 1983
QY 467 CCTCACCCGAAGCCAGCCACAAACTGCAAAAGCCACAGCTGTACCAACAGTAAAGAAA 526
Dd |||||
QY 1982 CCTCACCCGAAGCCAGCCACAAACTGCAAAAGCCACAGCTGTACCAACAGTAAAGAAA 1923
QY 527 GCGATGATAAGCCACAGAACATTACTACAGGCTGTGGTTCAAAGTCAAAAGATCC 586
Dd |||||
QY 1922 GCGATGATAAGCCACAGAACATTACTACAGGCTGTGGTTCAAAGTCAAAAGATCC 1863
QY 587 CTTTAAACAGAGTACTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACACAGATC 646
Dd |||||
QY 1862 CTTTAAACAGAGTACTTAAAGCGAATTAACCTTCCAAACAGCATAGATTCATACAGATC 1803
QY 647 GACTCTATCTCCTGTGGCTCTTGTGTCATCTTTGCCCTATAAAGTGAAGTCTGGTTTA 706
Dd |||||
QY 1802 GACTCTATCTCCTGTGGCTCTTGTGTCATCTTTGCCCTATAAAGTGAAGTCTGGTTTA 1743
QY 707 TACCACCTGCGCTCTGCTTCCCATATCAAAACCGCAGACAAACATACACTACTGGCTTATTG 766
Dd |||||
QY 1742 TACCACCTGCGCTCTGCTTCCCATATCAAAACCGCAGACAAACATACACTACTGGCTTATTG 1683
QY 767 CGGACATCATATGTGATATCATCTTACCTTTATGATATGCTATTATTCAGGCCAGACTCC 826
Dd |||||
QY 1682 CGGACATCATATGTGATATCATCTTACCTTTATGATATGCTATTATTCAGGCCAGACTCC 1623
QY 827 AGTTTGTAAAGAGGAGGAGACATAATA 852
Dd |||||
QY 1622 AGTTTGTAAAGAGGAGGAGACATAATA 1597

RESULT 10
ABU19457

DT	29-JAN-2004	(first entry)	
XX	Cyclic nucleotide gated channel alpha 1 coding sequence.		
DE	ss; gene; cyclic nucleotide gated channel alpha 1 ;		
XX	central nervous system; CNS; eye; blood-brain barrier;		
KW	blood-retina barrier; angiogenesis ; revascularisation;		
KW	retinal pigment epithelium; RPE; neurosensory retina ; choroidea ;		
KW	age-related macular degeneration; AMD; diabetic retinopathy;		
KW	Alzheimer's disease; Parkinson's disease; depression; bipolar disorder;		
KW	schizophrenia; amnesia; headache; stroke; insomnia; alcohol abuse;		
XX	anxiety; chronic pain; retinal blastoma; primary retinal detachment .		
OS	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	CDS	25..2097	
FT	/*tag= a		
FT	/product= "Cyclic nucleotide gated channel alpha 1"		
XX	WO2003087368-A2.		
XX	23-OCT-2003.		
XX	16-APR-2003; 2003WO-EP004003.		
XX	18-APR-2002; 2002EP-00008761.		
PR	05-DEC-2002; 2002US-0431173P.		
XX	(LYNK-) LYNKEUS BIO TECH GMBH.		
XX	Drumm K, Schloer SH, Goehring F;		
PI	WPI; 2003-845328/78.		
XX	P-PSDB; ADD93244.		
DR	Treating central nervous system and/or eye disorders comprises		
XX	administering to a subject a composition comprising a compound that		
PT	modulates a target gene or gene product, outside the blood-brain and/or		
PT	blood-retina barriers.		
XX	Claim 19; SEQ ID NO 1; 91pp; English.		
PS	This sequence encodes the human cyclic nucleotide gated channel alpha 1		
XX	protein. This cDNA may be targeted in the method of the invention for		
CC	treating a disorder of the central nervous system (CNS) and/or the eye.		
CC	The method comprises administering to a subject a composition comprising		
CC	a compound capable of modulating a target gene or gene product in a		
CC	therapeutic amount, where the composition is administered outside the		
CC	blood-brain and/or the blood-retina barriers. The composition is in a		
CC	designed form to be introduced into the cells or tissue of the CNS or eye		
CC	by a suitable carrier, characterized by the application occurring outside		
CC	the blood-brain or blood-retina barriers. It is also designed for		
CC	systemic administration or for administration by iontophoresis, or for		
CC	retrobulbar application or as eye drops. The compound, nucleic acid		
CC	molecule or vector is useful for the preparation of a composition for		
CC	treating, preventing and/or delaying a disorder of the CNS and/or the		
CC	eye, e.g. related to angiogenesis and/or neovascularisation, retinal		
CC	pigment epithelium (RPE), neurosensory retina and/or choroidea and wet		
CC	age-related macular degeneration (AMD) or diabetic retinopathy. The		
CC	compound may also be used as a lead compound in drug discovery and		
CC	preparation of drugs or prodrugs. The nucleic acid molecule and		
CC	polypeptide are also used for the validation of test substances, lead		
CC	compounds, drugs and prodrugs for the treatment of the disorder mentioned		
CC	above or for the identification and isolation of downstream genes, which		
CC	respond to modulation of a gene comprising the nucleic acid molecule or		
CC	its encoded gene product. The method is used for diagnosing, preventing		
CC	or treating the disorder cited above, which may include Alzheimer's		
CC	disease, Parkinson's disease, depression, bipolar disorder,		
CC	schizophrenia, amnesia, headache, stroke, insomnia, alcohol abuse,		
CC	anxiety, chronic pain, retinal blastoma, primary retinal detachment or		
CC	age-related macular degeneration.		
XX			

SQ	Sequence	2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;	
	Query Match	7.3%; Score 176.4; DB 10; Length 2500;	
	Best Local Similarity	49.6%; Pred No. 1.7e-28;	
	Matches	617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;	
QY	740	CAGACAACATACACTACTGGCTTATTGGGACATCATATGTGATATCATCTACCTTTTATG	799
Db	605	CTGATTACCTAGATATTGGCTCATTTTGGATTACCTATCAGACATAGCTATTATTAAATCG	664
QY	800	ATATCTCTATTATCCAGCCAGACTCCAGTTTGTGAAGGAGGAGACACATAATAGTGGATT	844
Db	665	ATATG---TTTGTACGAACAAGGACAGGTTACTTAAACAAGGAGCTGCTGGTAAAGGAAG	721
QY	860	CAATGAGCTAAGGAAACACTACAGGACTTCTACAAAATTTTCAGTTGGATGCGCATCAA	714
Db	722	ACTTTAAACTATAATAATAATAATCCAACTTGCAATTTTAAACTTGATGTTCTGTCTAC	781
QY	920	TAAATACCATTTGATATTGCTTACCTCTCTTTGGGTTTA---ATCCAATGTTTAGAGCAA	976
Db	782	TGATACCAACTGATTTGCTGTATTATTAAGTTAGGTGGAACCTATCCAGAAAATTAGATTAA	841
QY	977	ATAGGATGTTAAAGTACACTTCAATTTTGAATTTAATCATCATCACCCTAGAGTCTATAATGG	1036
Db	842	ACAGGTTGTTACGGTCTCTCGTATGTTTGAATTTCTCCAGAGAACAGAAAACAAGGACAA	901
QY	1037	ACAAAGCATATATCTACAGAGTTATTTCGAACAACCTGGGATACTTGTCTTTATTTCTGCACA	1096
Db	902	ACTATCCAAAACATCTTCAGGATTTCCAACTTGTATGTATATCGTCATCATTTATCCACT	961
QY	1097	TTAATGCCCTGTTTATTACTGGGCTTCAAACTATGAAGGAAATGGGCACTACTAGATGGG	1156
Db	962	GGATGCACTGTGTCTACTCTATTCTTAAAGCTATTGGGATTTGGAATGATACATCGG	1021
QY	1157	TGTA-----TGATGGGAAGGAACGAGTATCTGAGATGTT	1192
Db	1022	TCTACCTCGATATTAAATGATCCTGAAATTTGGCCGTTTGGCTAGAAAATACGTATACGCC	1081
QY	1193	ATTATTGGGCACTTCGAACCTTAAATTTACATTTGGTGGCTTCCAGAAACACAACTTTAT	1252
Db	1082	TTTACTGGTCTACACTGACTTTGACTACATTTGGTGAACACCCCTCCCGTGAGGGATT	1141
QY	1253	TTGAAATTTGTTTTCACACTCTTGAAATTTTTTTTGGAGTTTTTGTGTCTCCAGTTTAA	1312
Db	1142	CTGATATGCTCTTTGTGGTGTGATTTCTTAATTTGGAGTGTAAATTTTGTCTACCATCG	1201
QY	1313	TTGGTCAGATGAGATGTTGATTTGGAGCAGCTACAGCAATCAGNACTACTTCCCGCTT	1372
Db	1202	TTGGTAAACATAGGTTCTATGATTTTCCAAACATGAATGCGAGCCAGAGCAAAATTTCA	1261
QY	1373	GCATGGATGACACCACTTCCCTACATGAACAATTTACTCCATTTCTTAACTTGTGCAAAAG	1432
Db	1262	GAAATTGATGCTATCAAGCAATATATGCAATTTTCGAAATGTAAGCAAGATATGGAAGA	1371
QY	1433	GAGTTGGAATGTTGATGAATATACATGGGACTCTCAAAAGAAATGCTAGATGAGTCTGATT	1492
Db	1322	GGGTTATTAAATTTGTTTGAATCTGCTGACCTGGACCAACAAAAAAGAGTTGATGAGAAGA	1381
QY	1493	TGCTTAAGACCCCTACCACTACGGTCCAGTTTAGCCCTCGCCATTTGATGTGAATTTCA	1552
Db	1382	TCTTAAAGTATCTACCTCGATAAACCTAAGAGCAGAAAATTTGCCATCAACCTTCACTT	1441
QY	1553	TCATCAGCAAAAGTGCACCTTTGTTCAAGGGTTGTGTATACACAGATGATTTTATGACAT	1612
Db	1442	CATTAAAAAAGGTACCGCATTTTTCGTGATTTGTAAGCTGGTCTGTGTGGTGGATTTGCT	1501
QY	1613	TAAAGTTGAAATCCGTTCTCTCTATTGCTGTGTGACTTTTGTCTGCAAAAAGGAGAAATG	1672
Db	1502	TGAAATTTGCAACCCCAAGTCTACAGTCTCGAGATTAATTTTGCAGAAGAAAGGGGATAT	1561
QY	1673	GCAAGGAATCTATATCATCAAGCATGGAGAAAGTCCCAAGTTCTTTGGAGGCCCTGATGTA	1732
Db	1562	GACGAGAGATGTACATTTATCAAGGAAGGCAAACTCGCTGTGGTGGCAGATGATGAGTCA	1621

Qy	1733	CTAAGTTCTGGT-----TACTCTGAAGAAGTCGGGTGCGTGTTTTGGAGAAATC--AGCCTTC	1786
Db	1622	CTCAGTTTGTGGTATTGAGCGATGGCAGCACCTTCGGTGAGATCAGCATTTCTTAACATTA	1681
Qy	1787	TAGCAGCAGGAGGAGAAAACGTCGAACTGCCAATGTGCTGGCCACGCGTTTGCCCAATC	1846
Db	1682	AAGGGAGCAAGCTGGCAATCGAAGAACGGCCANATATAAAGTATTGGCTACTCAGACC	1741
Qy	1847	TTTTTAACTCTAGACAATAAAGACCCCTCCAAGAAATTTCTAGTGCATTATCCAGATTTCTGAAA	1906
Db	1742	TGTTCTGTCTCTCAAAGATGACCTCATGGAAGCTCTTAACTGAGTACCAGATGCCAAAA	1801
Qy	1907	GGATCCTCATGAAGAAACCGCAGTGTCTTTTAAAGCAGAGGCT	1950
Db	1802	CTATGCTAGAGAAATAAGGGAAGCAAAATTTTAAATGAAGATGGT	1845

RESULT 12

ADR24566
ID ADR24566 standard: DNA: 2500 BP.

AX
AC ADR24566;

21-OCT-2004 (first entry)

DE Breast cancer prognosis marker #427.

ds: breast cancer; prognosis; gene expression; diagnosis.

OS Homo sapiens.

PN WO2004065545-A2.

PD 05-AUG-2004.

PF 15-JAN-2004; 2004WO-US001100.

PR 15-JAN-2003; 2003US-00342887.

PA (ROSE-) ROSETTA INPHARMATICS LLC.

PA (NECA-) NETHERLANDS CANCER INST.

PI Van't Veer LJ, He Y;

DR WPI; 2004-593473/57.

Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.

PS Disclosure; SEQ ID NO 427; 226pp; English.

The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.

Sequence 2500 BP; 861 A; 431 C; 525 G; 683 T; 0 U; 0 Other;

Query Match 7.3%; Score 176.4; DB 13; Length 2500;

Best Local Similarity 49.6%; Pred. No. 1.7e-28;

Matches 617; Conservative 0; Mismatches 591; Indels 36; Gaps 5;

QY 740 CAGACAACATACACTACTGGCTTATTGCGGACATCATATGTGATATCATCTACCTTTATG 799

Db 605 CTGATTACCTAGAAATATTGGCTCATTTGGATTACGTATCAGACATAGTCTATTTAATCG 664

Qy 668 TGCTTGCTCACTCTTGCCCTATAACTGGAAC TGCTGGTTATACCACTGCGCCCTCGTCTTCC 727

Db 2 TGGTGTGTCCTATGCTTCTGCTAACAATCTGGGTGATATCTACCGCTTCCTCC 61
Qy 728 CATATCAAAACCGCAGACAATACATCTACTGCTTATTCGGGACATCATATGTGATATCA 787
Db 62 AGGAGATCAATCGGCGAAGCATCGCATTTGGTCTGTCTGAGCTACCTGTCCGACTTCC 121
Qy 788 TCTACCTTTATGATATGCTATTTATTCAGCCCGAGACTCCAGTTTGTGTAAGAGAGAGACA 847
Db 122 TGTATCTGATGATATCTGT---TCCACTTTCCGACCGGATACCTCGGAGGACGGGGTGC 178
Qy 848 TAATAGTGCATTCAAATGAGCTAAGAAACATACAGAGCTTCTACAAATTTTCAGTTGG 907
Db 179 TCGAGACGGACGCTTTGAAGCTGCGCACCCATACATGAAGCTCGAGATCTTCTACATCG 238
Qy 908 ATGTGCGCATCAATAATACCAATTTGATATTTGCTTACCTCTTCTTTGGGTTTAATCAATGT 967
Db 239 ACTGCTGTGCTGCTGCTGCTGCTTCTCTATTTGTTCCATCGGCTTTAACTCGATCC 298
Qy 968 TTAGAGCAAAATAGGATGTTAAAGTACACTTTCATTTTGTGAAATTAATCATACCTAGAGT 1027
Db 299 TCGCGAGCTTCGGCTGGTGAAGATCTACCGGTTCTGGGCTTCTATGATCGCACCGAGC 358
Qy 1028 CTATATAGACAAGATATATCTACAGAGTTATTCGAACAACCTGATACTTCTGCTTTTA 1087
Db 359 GGCACACCAACTACCCGAACTGTTCCGGAGCAGCGCCCTCATCTACCTGCTTGTGA 418
Qy 1088 TTTCTGACATTAATGCTGCTGTTTATTTACTTGGGCTTCAAACTATGAAGAAATGGCACTA 1147
Db 419 TATTCATTTGGAACGGTTGCTCTACCATCATCATACAGAACAATGGTTCGGATCAC 478
Qy 1148 CTAGATGGGT-----GTATGATGGGAAGAAACGAGTATCTGAGATGTT 1192
Db 479 GCAACTGGGTCTACCAGCACTCGGAGTCCGCGAGCTGGTCAAGAGTATCTCAGAGCT 538
Qy 1193 ATTATTTGGGAGTTTGAATTTTAACTTAACTTGGTGGCTTCCAGAACCAAACTTTAT 1252
Db 539 ACTACTGGTGCACCTGGCCCTGACCACTCGGGGATCTTCCCAAGCCGCGCTCCAAGG 598
Qy 1253 TTGAAATTTGTTTCAACTCTGAAATTTTCTGGAGTTTGTGTTCTCCAGTTAA 1312
Db 599 GCGAGTACGCTTTTGTATCTCGAGCTGCTTTTGGCTGATGCTCTTCGCCACCGGTAC 658
Qy 1313 TTGCTCAGATGAGAGATGTTGATTTGAGCAGCTACAGCCATCAGAACTACTTCCGCGCCT 1372
Db 659 TGGGCGACGTTGGCAACATTTGTCAGCTCAGTGTGAGTGCAGCGCGCAAGAGTTTCAAGCCA 718
Qy 1373 GCATGATGACACCATGTCCTACATGACAAATTAATCTTCCATCTTAACTTGTGCAAAAGC 1432
Db 719 AGCTGATGGCGTGAAGACGCTACATGCGGATGCGACGTTGCGGAAATCATCTCAGGTGA 778
Qy 1433 GAGTTCGGAATGCTGATGATATACATGCGGACTCTCAAGAAATGCTAGATGAGTCTGATT 1492
Db 779 AGGTTCATCAATGTTGCTGATCTGTGGCTTACGCAAAATATGCTCGGACGAGGCGCG 838
Qy 1493 TGCTTAAGACCCCTACCACTACGCTCCAGTTAGCCCTCGCCATTTGATGTGAATTCAGCA 1552
Db 839 CCGTGTCTCTCTCTGATAAATAAAGGCTGAATAGCAATTAAGCTCCATTAGATA 898
Qy 1553 TCATCAGCAAGTGCATCTGTTCAAGGGTTGTGATACAGATGATTTATGATGTTGC 1612
Db 899 CGCTCAAGCGGTTGAGATTTTCCAAACACAGAGGCGGCTTCTATGCGAACTGGTGC 958
Qy 1613 TAGATTTGAATCCGTTCTCTATTTGCTGCTGATCTTGTGCTCAAAAGGAGAAATTC 1672
Db 959 TGGCCCTTAGGCGCGTCTCTTCTGCGCCGCGACTACATCTCGAAGAGGCGAGGTGG 1018
Qy 1673 GCAAGGAAATGATATATCATCAAGCATGAGAAAGTCCAAAGTTCTTGGAGGCGCTGATGTA 1732
Db 1019 GCAAGGAGATCTACATTTGTGACCGAGGACGATTTGCAAGTGGTGGCCGAC---AATGAA 1075
Qy 1733 CTAAGTTCTGGTTATCTCTGAAAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1792

Db 1076 AGACGGTGATGGCTCCCTCCTGAAGGCTGCTTCTATTTTGGCAGATTAGTACTCAATA 1135
Qy 1793 CAGG---AGGAGGAAACCGTTCGAATGCTGCGTGGTGGCCACCGGTTTGGCAATCTTT 1849
Db 1136 TGGCAGCGCAGGCAACCGACGACAGCGAGCTTTCGCTCAGTGGGATACAGCGACCTCT 1195
Qy 1850 TAACTCTAGACAAAAGACCCCTTCCAAGAAATTTCTAGTGCATTTATCCAGATTTCTGAAGA 1909
Db 1196 TCGTCTGAGCAAGAGGACATGTGGACGCTCTGAAGAGTATCCGGGGCGCGTGTTC 1255
Qy 1910 TCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGGCTAAGACCGC 1958
Db 1256 GTCTGGAGTCTGATAGCTGCTCAGCGATTGGAGAAATACAAGAAGGCCCC 1304

RESULT 15

ADP56505

ID ADF56505 standard; DNA; 3027 BP.

XX ADF56505;

DT 12-FEB-2004 (first entry)

XX Modified rat olfactory cyclic nucleotide-gated ion channel DNA #1.

ds: gene; olfactory cyclic nucleotide-gated ion channel;
increased cAMP sensitivity; decreased cGMP sensitivity;
decreased nitric oxide sensitivity;
decreased calcium-calmodulin sensitivity.

OS Rattus norvegicus.

Key Location/Qualifiers
CDS 340..2334
/*tag= a

XX US2003157571-A1.

XX 21-AUG-2003.

XX 15-NOV-2002; 2002US-00295573.

XX 16-NOV-2001; 2001US-0332494P.

XX (COLS) UNIV COLORADO.

XX Karpen JW, Rich TC, Cooper DMF, Schaack J;

XX WPI; 2003-787336/74.

XX P-PSDB; ADF56501.

New nucleic acid encodes modified olfactory cyclic nucleotide-gated ion
channels which exhibit increased sensitivity and specificity for cAMP and
are useful to elucidate activities of proteins important in cAMP
signaling.

XX Disclosure; SEQ ID NO 1; 63pp; English.

The invention relates to an isolated nucleic acid encoding a modified
olfactory cyclic nucleotide-gated ion channel, where the channel
comprises mutations which together impart increased cAMP sensitivity.
CC decreased cAMP sensitivity; decreased nitric oxide sensitivity and
CC decreased calcium-calmodulin sensitivity. The invention is used to
CC elucidate activities of receptors, G-proteins, phospholipases, adenylyl
cyclases and other proteins important in cAMP signaling. The present
CC sequence represents modified rat olfactory cyclic nucleotide-gated ion
channel DNA.

XX Sequence 3027 BP; 783 A; 698 C; 746 G; 800 T; 0 U; 0 Other;

Query Match 5.5%; Score 133.2; DB 10; Length 3027;

Best Local Similarity 46.8%; Pred. No. 5.7e-19;

Matches 623; Conservative 0; Mismatches 673; Indels 36; Gaps 5;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 16:53:01 ; Search time 8615 Seconds
(without alignments)
13197.053 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 atgtttaaatcgtgacaaa.....aagaaagcgtgaagcaataa 2430

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
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2: gb_est2:*
3: gb_est3:*
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5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1707.4	70.3	2103	11	DQ043744 Homo sapi
2	1552.6	63.9	2103	11	DQ043745 Pan trogl
3	815.8	33.6	2056	4	AK040140 Mus muscu
4	553	22.8	553	2	BF725470 Bx16c03.Y
5	478	19.7	527	1	AL113036 DPEp686A
6	477.4	19.6	1947	4	CR626336 full-leng
7	470	19.3	655	2	BB635459 BB635459
8	457	18.8	3444	11	DQ032773 Homo sapi
9	430.2	17.7	437	2	BF725469 Bx16c03.x
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11	394.6	16.2	1455	8	DN691557 CGX77-A10
12	388.8	16.0	1377	8	DN679703 CGX07-F03
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15	333.8	13.7	3444	11	DQ032774 Pan trogl
16	322	13.3	1356	8	DN680109 CGX10-A08
17	320.8	13.2	468	1	AA069559 zf75a04.x
18	320.8	13.2	656	3	BP224184 BP224184
19	308.4	12.7	737	8	DN900758 naql0c08
20	308.4	12.7	978	3	BQ068992 AGENCOURT
21	304	12.5	633	7	CK619966 mk30e03.Y
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ALIGNMENTS

RESULT 1
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LOCUS Homo sapiens CNGB3 gene, VIRTUAL TRANSCRIPT, partial sequence.
DEFINITION Homo sapiens CNGB3 gene, VIRTUAL TRANSCRIPT, partial sequence.
ACCESSION DQ043744
VERSION DQ043744.1 GI:66894959
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and Chimpanzees
JOURNAL (er) PLoS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Gnanowski,S., Sackton,T.B., Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment. Translation starts at the beginning of alignment.
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/chromosome="8"
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ORIGIN
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Best Local Similarity 81.2%; Pred. No. 0;
Matches 1708; Conservative 0; Mismatches 395; Indels 0; Gaps 0;

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24 280.8 11.6 738 3 BT736222
c 25 280 11.5 423 3 BM938767
26 279 11.5 445 8 H53423
27 277.6 11.4 747 7 CR376265
28 271.2 11.2 545 1 AW465556
29 262.2 10.8 563 2 BG304577
c 30 261.6 10.7 503 1 A1150392
31 259.8 10.7 716 8 CX353216
c 32 236.8 9.7 1238 8 DN682911
33 234 9.6 247 1 AA317961
34 232.4 9.6 270 1 AA012972
35 224 9.2 325 2 BE982488
36 219.6 9.0 823 7 CO814239
c 37 219 9.0 696 5 BW269181
38 216.2 8.9 518 1 AV605886
c 39 216.2 8.9 747 3 BT733974
40 212.4 8.7 215 1 AA069498
41 211 8.7 869 6 CD327412
42 207.4 8.5 873 8 CX828680
43 201.6 8.3 979 5 BX370500
44 197.2 8.1 581 1 AV605887
c 45 193.4 8.0 1290 8 DN691556

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CR376265 CR376265
AW465556 BP230019A
BG304577 f188b05.Y
A1150392 qf40g11.x
CX353216 s8a1yb52
DN682911 CXK26-H06
AA317961 EST20020
AA012972 z63b03.f
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DB |||||
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DB |||||
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DB |||||


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LOCUS
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ACCESSION
  DQ043745
VERSION
  DQ043745.1 GI:66894960
KEYWORDS
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SOURCE
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ORGANISM
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REFERENCE
  1 (bases 1 to 2103)
  Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
  Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Cividello, D.,
  White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
  A Scan for Positively Selected Genes in the Genomes of Humans and
  Chimpanzees
  (er) PLOS Biol. 3 (6), E170 (2005)
  15869325
REFERENCE
  2 (bases 1 to 2103)
  Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B.,
  Hubisz, M.J., Fiedel-Alon, A., Tanenbaum, D.M., Cividello, D.,
  White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
  Direct Submission
  Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
  Rockville, MD 20850, USA
COMMENT
  This sequence was made by sequencing genomic exons and ordering
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[illegible]

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QY 2336 CTTCTCGTCAATCACTATTATCAGATGGCTCTTCTGCTAGGCGGAGAGAGAGTTTC 2395
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RESULT 4

BF725470

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BF725470 553 bp mRNA linear EST 05-JAN-2001
bx16c03.y1 Human Iris cDNA (Un-normalized, unamplified): BX Homo
sapiens cDNA clone bx16c03 5', mRNA sequence.

BF725470
BF725470.1 GI:12041381

EST.
Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 553)

Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.

NEIBANK: EST analysis and bioinformatics for ocular genomics

Invest. Ophthalmol. Vis. Sci. 41 (2000) in press

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 16 row: c column: 03

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1..553

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/lab_host="EMDH10B"

/clone_lib="Human Iris cDNA (Un-normalized, unamplified):

BX"

/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris

tissue was pooled from 10 individuals ranging in age from

4-80 years and RNA was extracted. From this pooled sample

an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A

directionally cloned cDNA library in the pCMVSPORT6 vector

was constructed at Life Technologies, essentially

following the protocols of the SuperScript Plasmid System

full details of which are contained in the manufacturer's

instruction manual (<http://www.lifetech.com/>). First

strand synthesis was carried out using a Not I

primer-adaptor

[5'-PGACTAGTTCTAGATCGGAGCGGCCGCC(T)15-3']. Not I/blunt

end inserts were cloned into the Not I/EcoR V sites in the

vector. EST analysis was performed on the unamplified

library at the NIH Intramural Sequencing Center (NISC).

ORIGIN

Query Match

Best Local Similarity 22.8%; Score 553; DB 2; Length 553;

100.0%; Pred. No. 1.1e-117;

AUTHORS
TITLE
JOURNAL

COMMENT

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QY 1701 AGAAGTCCAAAGTTCTTGGAGGCCCTGATGTTAAAGTTCTGTTTACTTCTCAAGCTGG 1760

Db 844 GCAAGTGCAGGCTTGGGGCGCCCTGATGGGAATCTGTCTGCTGACCGCTGAAGCTGG 903

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QY 1821 TGTGTGCGCCACGGGTTTGGCAATCTTTTAACTCTAGACAAAGAACCTCTCAAGAAAT 1880

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QY 1881 TCTAGTGCATTATCCAGATTTCTGAAGGATCTCATGAAGAACCCAGAGTCTTTTAA 1940

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 DEFINITION BB635459
 ACCESSION BB635459
 VERSION BB635459.1 GI:16471509
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 655)
 AUTHORS Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T.,
 Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J.,
 Kanno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K.,
 Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K.,
 Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
 Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F.,
 Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.
 RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
 Unpublished (2001)
 TITLE Contact: Yoshihide Hayashizaki
 JOURNAL Laboratory for Genome Exploration Research Group, RIKEN Genomic
 COMMENT Sciences Center(GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22, Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/
 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
 Itoh,M., Kanno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 waki,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
 Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
 Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.
 and Hayashizaki,Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Kanno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P.,
 Sugahara,Y. and Hayashizaki,Y.

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. *Genome Res.* 11 (2), 281-289 (2001)

Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamana, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. *Mamm. Genome* 12, 673-677 (2001)

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

e mouse tissues.

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FEATURES
source
Location/Qualifiers
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/organism="Mus musculus"
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thymus"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. cDNA went through one round of normalization
to Rot = 10.0 and subtraction to Rot = 459.0. Second
strand cDNA was prepared with the primer adapter of
sequence [5' GAGAGAGAGATCTCGATTAAATTAATCCCCCCCCCCC
3']. cDNA was cleaved with XhoI and BamHI. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
FLC I"

```

ORIGIN	Query Match	19.3%	Score 470;	DB 2;	Length 655;
	Best Local Similarity	84.2%;	Pred. No. 2.4e-98;		
	Matches 553;	Conservative	0;	Mismatches 101;	Indels 3;
	Gaps	2;			
Qy	1078	TTGCTGTTTATTCTGCACATTAATGCCCTGTGTTTATTACTGGGCTTCAAACCTATGAAGGA	1137		
Db	1	TTGCTGTTTCTCTCGCACATTAACGCCTGTGTTTATTACTGGGCTTCAGACTATGAAGGA	60		
Qy	1138	ATTGGCACTACTAGATGGGTGTATGATGGGGAGGAAACGAGTATCTGAGATGTTATTAT	1197		
Db	61	ATTGGCTCAACTAAATGGGCTCTAATATGGTGAAGGCAACAAGTATCTCGATGCTTTTAT	120		
Qy	1198	TGGGCAGTTTCGAACCTTTAAATACCATTTGGTGGGCTTCAGAAACAAACCTTTATTTGAA	1257		
Db	121	TGGGCAGTTTCGAACCTTTAAATACTATCGGGGGGCTTCAGAGGCACAGACTTCATTTTGA	180		
Qy	1258	ATTGTTTTTCAAACCTCTTGAATTTTTTTCTCGAGTGTTCCTCCAGTTTAAATTTGGT	1317		
Db	181	ATTGTTTTTCAAATCTTGAATTTTTTCTCGGGGTTTTGTTTTCTCCAGCTTAATTTGGT	240		
Qy	1318	CAGATGAGAGATGTGATTGGAGCAGCTPACAGCCAAATCAGAACTACTTCCCGGCTGCATG	1377		
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Qy	1378	GATTGACACCAATTGCTACATGAAACAAATTTACTCCAAATCCTTAAACTTTGTGCAAAAGCCAGTT	1437		
Db	301	GACCAATATCATTTGCCTACATGAACAAATATCTATTCTCAGAGTGTGCAGTATCCGATTT	360		
Qy	1438	CGGACTTTGGTATGAATATACATGGGACTCTCAAAGAAATGCTAGATGAGTCTGATTTGCTTT	1497		
Db	361	CGGACTTTGGCTGGAATATACATGGAATCTCAAAAGAAATCTTAGATGAGTCCAACTTGCCTT	420		

Qy	1498	AAGACCTCAACACTAGCGTTCAGTTAGCCCTCGCCATTTGATGTGAACCTTCAGCATCATC	155
Db	421	GAGAACCTCCGACAGCAATGCGAGTTGTCTATTTCGCCCTTGACATAAACTTCAGTATCATC	480
Qy	1558	AGCAAGTCGACATTGTTTCAAGGGTGTGTATACACAGATGATTTATGACATGTTGCTTAAGA	1617
Db	481	GACAGGTGGAGTTATTCAAGGCTGTGACACACAGATGATTTATGACCTGCTGCTTAAGA	540
Qy	1618	TTGAAATCCGTTCTCTATTATTTTGCCTGGTGACTTTGTCTGCAAAAAGGAGAAATTTGCCAAG	1677
Db	541	TTGAAATCCCACTATTATTATTTTACCTGGTGACTGTTGCTGCAAAAAGGAGAAATTTGGAAG	600
Qy	1678	GAATGTATATCATCAAGCATGAGAAAGTCCAAGTTCTTTGGAGGCCCTGATGTACT	1734
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RESULT 8			
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DEFINITION		Homo sapiens CNGB1 gene, VIRTUAL TRANSCRIPT, partial sequence,	
		genomic survey sequence.	
ACCESSION		DQ032773	
VERSION		DQ032773.1	GI:66883982
KEYWORDS		GSS.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
		Hominidae; Homo.	
REFERENCE		1 (bases 1 to 3444)	
AUTHORS		Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.R.,	
		Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D.,	
		White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE		A Scan for Positively Selected Genes in the Genomes of Humans and	
		Chimpanzees	
JOURNAL		(er) PLOS Biol. 3 (6), E170 (2005)	
PUBMED		15869325	
REFERENCE		2 (bases 1 to 3444)	
AUTHORS		Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.R.,	
		Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D.,	
		White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.	
TITLE		Direct Submission	
JOURNAL		Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,	
		Rockville, MD 20850, USA	
COMMENT		This sequence was made by sequencing genomic exons and ordering	
		them based on alignment. Translation starts at the beginning of	
		alignment.	
FEATURES		Location/Qualifiers	
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		/chromosome="16"	
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Best Local Similarity		51.1%;	Pred. No. 3,6e-95;
Matches		688; Conservative	0; Mismatches 659; Indels 0; Gaps 0;
Qy	617	TTCAAACAGCATAGATTTCATACAGATCGACTCTATCTCTGTGGCTTCTGCTTGTCTA	676
Db	1913	TTCCCCAGAGCATTCACCCGCTGACCAANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1972
Qy	677	CTCTTGCCATATACTGGAAGTCTGGTTTATACCAGCTGCGCTCTGCTTCCCATATCAA	736
Db	1973	NN	2032
Qy	737	CCGACAGACAATACACTACTGGCTTTATTTCGGGACATCATATGTGATATCATCTACTCTT	796

[illegible]

Qy 1877 AATTTCTAGTGCATTATTCAGATTCTGAAGGATCTCATGAAGAAAGCCAGAGTCTTTT 1937
 Db 3173 AGATTTTGGTGCATTTATCTCTGAGTCTCAGAAAGTTACTCCGGAAGAAGCCAGCGCATGC 3232
 Qy 1937 TAAAGCAGAAGGCTTAAGACCGCAGAAG 1963
 Db 3233 TGAGAGCAACAATAGCCCAAGGAGG 3259

RESULT 9
 BF725469/c
 LOCUS
 DEFINITION bx16c03.x1 Human Iris cDNA (Un-normalized, unamplified): BX Homo sapiens cDNA clone bx16c03 3', mRNA sequence.
 BF725469
 ACCESSION BF725469.1 GI:12041380
 VERSION
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 437)
 Wistow, G.J., Bernstein, S., Behal, A. and Smith, D.
 NEIBANK: EST analysis and bioinformatics for ocular genomics Invest. Ophthalmol. Vis. Sci. 41 (2000) In press
 CONTACT: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 16 row: c column: 03
 Seq primer: -21M13 forward primer (ABI).
 Location/Qualifiers
 1..437
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 /mol_type="mRNA"
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 /dev_stage="Adult"
 /lab_host="EMDH108"
 /clone_lib="Human Iris cDNA (Un-normalized, unamplified): BX"
 /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris tissue was pooled from 10 individuals ranging in age from 4-80 years and RNA was extracted. From this pooled sample an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A directionally cloned cDNA library in the pCMVSPORT6 vector was constructed at Life Technologies, essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's Instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor
 [5'-pGACTAGTTCTAGATCCGAGCGGCCCC(T)15-3']. Not I/blunt end inserts were cloned into the Not I/EcoR V sites in the vector. EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."
 ORIGIN

Query Match 17.7%; Score 430.2; DB 2; Length 437;
 Best Local Similarity 99.3%; Pred. No. 4.3e-89;
 Matches 432; Conservative 0; Mismatches 3; Indels 0; Gaps 0

Qy 1759 GGGTCGGGTGTGGAGAATCAGCCCTTCTACGACGAGGAGGAAACCGTCGAAGTCCC 1818
 Db 437 GGGTCGGGTGTGGAGAATCAGCCCTTCTACGACGAGGAGGAAACCGTCGAAGTCCC 378
 Qy 1819 AATGTGGTGGCCCGCGGGTGTGGCCAATCTTTTAACTCTAGACAAAAAGACCTCCAAAG 1878

|||||
Db 377 AATGTGGTGGCCACGGGTTTGCCAACTCTTTAACTCTAGACAAAAGACCCCTCCAAGAA 318
|||||
Qy 1879 ATTCTAGTGCATTATCCAGATTCTGAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTA 1938
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Db 317 ATTCTAGTGCATTATCCAGATTCTGAAGGATCCTCATGAAGAAAGCCAGAGTGCTTTTA 258
|||||
Qy 1939 AAGCAGAGGCTAAGACCCGAGAGCAACCCCTCCAAGAAAGATCTTGCCTCTCTTC 1998
|||||
Db 257 AAGCAGAGGCTAAGACCCGAGAGCAACCCCTCCAAGAAAGATCTTGCCTCTCTTC 198
|||||
Qy 1999 CCACCGAAGAGAGACACCCAACTGTTTAAACTCTCTAGGAGGCACAGAAAGCA 2058
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Db 197 CCACCGAAGAGAGACACCCAACTGTTTAAACTCTCTAGGAGGCACAGAAAGCA 138
|||||
Qy 2059 AGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAGCTCAGAAAGAAAGAAATCT 2118
|||||
Db 137 AGTCTTGCAGACTACTCAAATTTGAAGCGAGAGCAGCTCAGAAAGAAAGAAATCT 78
|||||
Qy 2119 GAAGGAG 2178
|||||
Db 77 GAAGGAG 18
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Qy 2179 CAAAAGAGAAATCAA 2193
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Db 17 CAAAAAAGAAAAA 3

RESULT 10
BE287002
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM8547 row: i column: 08
High quality sequence stop: 774.
Location/Qualifiers
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/lab_host="DH108"
/clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: SalI;
Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"

FEATURES
source

RESULT 11
DN691557
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
DN691557 1455 bp mRNA linear EST 30-MAR 2004
CGX77-A10.y1d-s SHGC-CGX Gasterosteus aculeatus cdna clone
CGX77-A10 5', mRNA sequence.
DN691557
DN691557.1 GI:62046053
EST.
Gasterosteus aculeatus (three spined stickleback)
Gasterosteus aculeatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorphi; Acanthopterygii; Percomorpha; Gasterosteiformes;
Gasterosteidae; Gasterosteus.
1 (bases 1 to 1455)

AUTHORS	TITLE	JOURNAL	COMMENT
Kingsley,D.M., Peichel,C., Balabhadra,S., Grinwood,J., Dickson,M., Schmutz,J. and Myers,R.M.	Expressed sequence tags from <i>Gasterosteus aculeatus</i>	Unpublished (2003)	
Contact: Grinwood, Jane			
Stanford Human Genome Center			
Stanford University School of Medicine			
975 S California Ave, Palo Alto, CA 94304, USA			
Tel: 650 320 5917			
Fax: 650 320 5801			
Email: jane@shgc.stanford.edu			
Plate: 77			
High quality sequence start: 18			
High quality sequence stop: 941.			

FEATURES
SOURCE

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1. 1455
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/sex="mixed male and female".
/tissue_type="eyes"
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CGX"
/notes="Vector: Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodt sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTAGTCTCAGATCGCAGCGCCGCC(T)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5 prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving a junction of the form
'xxxATC' (where is ATC is the second half of the EcoRV
site, and xxx is derived from the cDNA sequence). A map of
the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
http://www.openbiosystems.com/stickleback"

```

ORIGIN

Query Match	16.2%	Score 394.6	DB 8	Length 1455
Best Local Similarity	61.9%	Pred. No. 1.1e-80		
Matches 641	Conservative 0	Mismatches 389	Indels 6	Gaps 1
Qy	809	TTATCCAGCCAGACTCCAGTTTCTAGAGGAGGAGACATAATAGTGGATTCAAATGAGC	868	
Db	39	TTTGGCAGCCCGCTCAGTPTTCTCATGCGGAGAGCGTTATTAAAGCGGACCTATGG	98	
Qy	869	TAAGAAACACTACGAGACTTCTACAAAAATTTTCAGTTTGGATGTCGCATCAATAATACCAT	928	
Db	99	CTAAGTATTTTATCGGNAATCCCAACGATTTAGATTGATATCTCAGCGTCTGCGCCT	158	
Qy	929	TTGATATTTGTACTCTCTTTCGGGTTTAAATCCAAATGTTTAGAGCAAAATAGGATGTTAA	988	
Db	159	TTGACCTTCTCGGCGTGTACTTTTGAGTTCTCGGCGGTATACAGAGTCAACCGCTTTATCA	218	
Qy	989	AGTACACTTCAATTTTGTGAATTTTAATCATCACCTAGAGTCTATAATCGACAAGCATATA	1048	
Db	219	GGATTGAGTCCCTTCTTGTGACTTTTAGTGATCGACTCGAGAGCATCATGGCCAAAGCCCTACA	278	
Qy	1049	TCTACAGAGTTATTTCGAACAACCTGGATCTTGCTGTTTATTTCGCACATAATGCGCTGTG	1108	
Db	279	TCTGGAGAGTGATTTCGCACCAAGGTACCTGCTCTTCCTGGCCCTCCATCTCAACAGCTGTG	338	
Qy	1109	TTTATTACTGGGCTTCAAACATCAAGAGGAATTTGGCACTACTAGATGGGTGTATGATGGG	1168	

Db	339	CGTACTAGCTGCTCCATGTAACGGGTATTAAGTCGACACCGTGGGTGATAAATGGAG	398
Qy	1169	AAGGAAACAGGATATCTGAGATGTTATTATTTGGGCAGTTTCGAACCTTTAAATTTACCAATTTGGTG	1228
Db	399	AGGGCAGCGCGTACCTGCTGTTGTTACTACTACGACGTCGCCAGTCTGATCAACATCGGTG	458
Qy	1229	GGCTTCAGAACCAACAACTTTATTTGAAATTTGTTTTTCAACTCTTTGAAATTTTTTTTTTCTG	1288
Db	459	GTCTTCAGAGCCATTAACCACTTCGAGATATCTTTTTTTCAGATGGGCAACTTTTTTCATTG	518
Qy	1289	GAGTTTTTCTGTTCTCCAGTTTAATTTGGTCAGATGAGAGATGTGATTTGGAGCAGCTACAG	1348
Db	519	GGTTTTTGTATTCTCCAGTTTTCAGGGCATCCATGATGGCTGTGTTGACTACATGAATACCTACA	578
Qy	1349	CCAATCAGAACTACTTCCGGCGCTGCATGGATGACACCAATTGGCTACATGAACAAATTTACT	1408
Db	579	CGGGGAAGACCTATTTCAGGGCATCCATGATGGCTGTGTTGACTACATGAATACCTACA	638
Qy	1409	CMATTCCTAAACTTTGTGCAAAAGCGAGTTTCGGACTTGGTATGAATATACATGCGACTCTC	1468
Db	639	ATATCCCAAGGTGTTTCAGAACAGAAATCCGGACCTGGTACAACACTACCTGGTCAGCTC	698
Qy	1469	AAAGATGCTAGATGAGTCTGATTTCGTTTAAAGACCTACCAACTACGGTCCAGTTAGCCC	1528
Db	699	AGGGCATGCTGGACGAGTCGGAGCTGCTAGACAAGATGCCCTCTGGTGATGAACATGCCA	758
Qy	1529	TCGCCATTGATGTGAACCTTCAGCATCATCAGCAAAAGTCGACTTGTTCACAGGGTTGTGATA	1588
Db	759	TCGCGCTGGACATCAACTTGTCAACCTTCAGAAAGATTGCAATTTTCAGGGCTGTGACC	818
Qy	1589	CACAGATGATTTATGATGTTGCTTAAGATTTGAAATCCGTTCTCTATTTGCCTGGTGACT	1648
Db	819	AGCAGATGTTTGGTGGATATGTTCTGAGGCTCAAGTCAATTTGTCTACTCTCCCGGAGACT	878
Qy	1649	TTGCTCTGCAAAAGGGAGAAATTTGGCAAGAAATGTATATCATCAACCATGGAGAGTCC	1708
Db	879	TTGTTTGTAAAGAAAGCGACATCGGNTAAGAGATGTACGTGATCAAAAGTTGGTCGGTGCC	938
Qy	1709	AAGTTCTTTGAGAGCCCTGATGGTACTAAAGTTCTTGGTTTACTCTGAAAGCTGGGTGGTGT	1768
Db	939	ANGTGGTGGAGACCTGACAAAGCATCGTGTTCGTACGCTGAAGCCGGCTCGCTNG	998
Qy	1769	TTGGAGAAATCAGCCTTTCTA-----GCACGAGGAGGAGAAACCGTGGAACTGCCCAATG	1828
Db	999	TCGGAGAAATCAGTTTGTCTACAGTCTGCTAANGATGGANGAAACAGCGCACAGCTAATG	1058
Qy	1823	TGGTGGCCACGGGTT	1838
Db	1059	TGAAAGCTCACGGGTT	1074
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LOCUS			linear
DEFINITION			EST 30-MAR-2005
			CGX07-F03.5.yid-s SHGC-CGX Gasterosteus aculeatus cDNA clone
			CGX07-F03 5', mRNA sequence.
ACCESSION			
VERSION			DN679703.1 GI:62021754
KEYWORDS			EST.
ORGANISM			Gasterosteus aculeatus (three spined stickleback)
			Gasterosteus aculeatus
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
			Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
			Acanthomorpha; Acanthopterygii; Percomorphia; Gasterosteiformes;
			Gasterosteidae; Gasterosteus.
			1 (bases 1 to 1377)
REFERENCE			Kingsley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M.,
AUTHORS			Schmutz,J. and Myers,R.M.
			Expressed sequence tags from Gasterosteus aculeatus
TITLE			Unpublished (2003)
JOURNAL			Contact: Grimwood, Jane
COMMENT			Stanford Human Genome Center

Stanford University School of Medicine
975 S California Ave, Palo Alto, CA 94304, USA
Tel: 650 320 5917
Fax: 650 320 5801
Email: jane@shgc.stanford.edu
Plate: 07
High quality sequence stop: 816.

FEATURES

source

1. .1377

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/clone_lib="SHGC-CGX"
/notes="vector: Express 1; Total and poly A+
isolated from the indicated stickleback T1 phage
library was constructed in the Express 1 plasmid
Open Biosystems. First strand cDNA synthesis
with an 54 bp linker primer containing an
overhang complementary to the NotI site (first
preceded by a synthetic NotI site (first
5'-GACTAGTCTAGATCGAGCGGCCCTT25-3').
cDNA libraries were made in the Express 1
second strand synthesis, cDNAs were made blunt
corresponding to the original 5 prime end and
cloned directionally into the NotI and EcoRV
sites of the Express 1 vector. The EcoRV
Express 1. Note that the EcoRV site is typically
in the blunt end cloning, leaving a junction
'xxxATC' (where ATC is the second half of the
NotI site, and xxx is derived from the cDNA
sequence). The Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_q.
q.php#8 The primary library was transferred
from DH10B (T1 phage resistant) bacteria. Clones
from Open Biosystems:
http://www.openbiosystems.com/stickleback"

```

ORIGIN

Query Match	16.0%;	Score 388.8;	DB 8;	Length 1377;
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Matches 595; Conservative	0;	Mismatches 324;	Indels 3;	Gaps 1;
QY	1128	CTATGAAGGAATTGGCCACTACTAGATGGGTGTATGATGGGGAAGGAACACGAGTATCTGAG	1187	
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QY	1188	ATGTTTATATTGGGCAGTTCCGAATTTTAAATTACCATTTGGTGGCTTCCGAACCCACAAC	1247	
Db	61	CTGTTACTACTTTTGGCGGTGAAGACATTTGATCACCATCGGAGGACTTCTCTGACCCACCAC	120	
QY	1248	TTTATTTTGAAATGTTTTTCAACTCTTGTAAATTTTTTTCTGGAGTTTTTGTGTCTCCAG	1307	
Db	121	CGTCTTTGAGATCTGCTTCCAGCTCATCAACTACTTTCGTTGGGGTCTTTGCCCTTTTCGAT	180	
QY	1308	TTTAAATTGGTTCAGATGAGAGATGTGATTTGGAGCAGCTTACAGCCAATCAGAACTACTTCCG	1367	
Db	181	CATGATCGGCACATGAGAGATGTGGTTCGAGTCTGGACCCGCCGGAGAGAATCTACTACCG	240	
QY	1368	CGCCTCGATGGATGACACCAATTCGCCTACATGAACAATTTACTTCATTTCTTAAACTTTGGCA	1427	
Db	241	AGCCTCGATGGACAGCACCAATCCAGTACATGAATCTTTACCAATCCCGGACAGGTCCA	300	
QY	1428	AAAGCGAGTTTCGGACTTGGTATGAAATATACATGGGACTCTCAAAGAAATGCTAGATGATC	1487	
Db	301	GAACCGCATCAAGACCTGGTACGACTACACTTGGAGATCCAGGGCATGCTGATGNACA	360	
QY	1488	TGATTTGCTTAAAGCCCTACCAACTACGGTTCAGTTAGCCCTCGCCANTTGATGTGAACCTT	1547	
Db	361	GGAGCTTCTAGTGCAGCTTCCCGCTAAGATGAGGCTGGCATGGCTGTGACGCTCAACTA	420	

	Qy	1548	CAGCATCATCAGCAAAAGTCACCTGTTTCAAGGGTTGTGTATACACAGATGATTATATGACAT	1607
	Db	421	CTCCATCGTCAGCAAAAGTGCCCTTGTTCAGGGCTGTGCACAGACAGATGGTGTTCGAACCT	480
	Qy	1608	GTTTGCTAAGATTTGAAAATCCGTTCTCTATTTCGCCGTGGTGACTTTGTCTGCAAAAGAGCAGA	1667
	Db	481	GCTGACGAGGCTCAAGTCAGTCGTCTACCTGCCCGGAGACTTTTGTCTGTAAAGAGGCGGA	540
	Qy	1668	AATTGGCAAGGAATAATGTATATCATCAAGCATAGGAGAAGTCCAAGTTCTTTGGAGGCCCTCGA	1727
	Db	541	GATCGGCAGGGAGATGTATCATCATTAACAAGGGGAGGTTTCAGGTGGTCGGAGGTCCAGA	600
	Qy	1728	TGTTACTAAAGTTCTTGTTTACTCTGAAGAGCTGGTGGTGTGTTTTGGAGAAATCAGCCTTCT	1787
	Db	601	CTTGACAGCCGTTGTTTGTACCATCAGATCTGGTGTCTGTGTTTGGAGAGATCAGTTTGCT	660
	Qy	1788	AGCAGCAGGAGGAGGAAACCGTCGAACTGCCAATATGGTGGCCCCACGGGTTTGCCCAATCT	1847
	Db	661	GGCAGGAGGAGGGGGAACCGACGGACCGCCAACGTGAAGTGCACGGATTTGCCAACCT	720
	Qy	1848	TTTAACTCTAGACAAAAAGACCTCCAGAAATTTCTAGTGCATTTCCAGATTTCTGAAG	1907
	Db	721	GTTTCATCTCGATTAAGAAGAAGTGTGGCAGAAATCTTAGTGAACCTACCCAGAGTCCCAGAA	780
	Qy	1908	GATTCCTCATCAAGAAAGCCAGAGTGCTTTTAAAGCAGAAGGCTTAAGACCCGACGAAGCAAC	1967
	Db	781	GCTCCTCCGCAAGAAAGCCAAAGACCATTGTT--GACTAAGGACAGAGCCAGAGAGAA	837
	Qy	1968	CCCTCCAGAAAAAGATCTTGCCCTCTCTTCCACCGAAAGAGAGACACCCAACTGTT	2027
	Db	838	AGSTGGAGCCAAAGAGGCTGTGCAGATTATTCACCGCAGACCAGACACACCCGAGATGTT	897
	Qy	2028	TAAACTCTCTTAGGAGGCACA	2049
	Db	898	NCAGGGCGCTCTGAANGTCTCA	919
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RESULT 13				
DN686265			1140 bp mRNA linear EST 30 MAR 2004	
LOCUS				
DEFINITION			CGX46-A07.yid-s SHGC-CGX Gasterosteus aculeatus cDNA clone	
ACCESSION			CGX46-A07.5, mRNA sequence.	
VERSION			DN686265	
KEYWORDS			EST.	
SOURCE			DN686265.1 GI:62035421	
ORGANISM			Gasterosteus aculeatus (three spined stickleback)	
			Gasterosteus aculeatus	
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
			Actinopterygii; Neoceratrygii; Teleostei; Euteleostei; Neoteleostei;	
			Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;	
			Gasterosteidae; Gasterosteus.	
REFERENCE			1 (bases 1 to 1140)	
AUTHORS			Kingley,D.M., Peichel,C., Balabhadra,S., Grimwood,J., Dickson,M., Schmutz,J. and Myers,R.M.	
TITLE			Expressed sequence tags from Gasterosteus aculeatus	
JOURNAL			Unpublished (2003)	
COMMENT			Contact: Grimwood, Jane Stanford Human Genome Center Stanford University School of Medicine 975 S California Ave, Palo Alto, CA 94304, USA Tel: 650 320 5917 Fax: 650 320 5801 Email: jane@shgc.stanford.edu Plate: 46 High quality sequence stop: 764. Location/Qualifiers 1..1140 /organism="Gasterosteus aculeatus" /mol_type="mRNA" /strain="Conner Creek sticklebacks, WA USA" /db_xref="taxon:69293" /clone="CGX46-A07" /sex="mixed male and female"	
FEATURES				
source				

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/tissue_type="eyes"
/dev_stage="adult"
/lab_host="DH10B (T1 phage resistant)"
/clone_lib="SHGC-CGX"
/notes="Vector: Express 1; Total and poly A+ RNA was
isolated from the indicated stickleback tissue, and a cDNA
library was constructed in the Express 1 plasmid vector by
Open Biosystems. First strand cDNA synthesis was primed
with an 54 bp linker primer containing an oligodT sequence
preceded by a synthetic NotI site (first strand primer:
5'-GACTAGTCTAGATCGGAGCGGCCCTT)25-3'). Following
second strand synthesis, cDNAs were made blunt at the end
corresponding to the original 5' prime end of mRNA, and
cloned directionally into the NotI and EcoRV sites of
Express 1. Note that the EcoRV site is typically destroyed
in the blunt end cloning, leaving a junction of the form
'xxxATC' (where ATC is the second half of the EcoRV
site, and xxx is derived from the cDNA sequence). A map of
the Express 1 vector is available at:
http://www.openbiosystems.com/cdna_library_construction_fa
q.php#8 The primary library was transformed and amplified
in DH10B (T1 phage resistant) bacteria. Clones available
from Open Biosystems:
http://www.openbiosystems.com/stickleback"
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ORIGIN

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Query Match 15.4%; Score 373.4; DB 8; Length 1140;
Best Local Similarity 61.5%; Pred. No. 8.9e-76;
Matches 649; Conservative 0; Mismatches 402; Indels 5; Gaps 3;
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Qy 617 TTCCAAACAGCATAGATTCATACAGATCGATCTATCTCTGTGGCTCTTCGTGTCA 676
Db 83 TCCCTTCAGCATGACCGCTTCACTGATGTATACGTGGTCTTCTGTGTGG 142
Qy 677 CTCCTTGCTATACTGAACTGCTGTGTATACCACTGCGCTCTCTCCCATATCAAA 736
Db 143 TGGGGCTGGAAGTGGAGTGGTGTGATTCGGGGCGGGGGCTTCCATACCAA 202
Qy 737 CCGCAGACAACATCACTACTGCTTATTCGGGACATCATATGTGATATCATCTT 796
Db 203 CCCCAGAGACCTTCACCTGTGGCTCTCTGTGGACTACCTGTGACCTGATCATCA 262
Qy 797 ATGATATGCTATTATCCAGCCAGACTCCAGTTTGAAGAGGAGGAGATATAGTGG 856
Db 263 CTGACATCTGCTGATGACGCCCGCTTCACTGTGTTGTCGAGGAGGAGACATTTG 322
Qy 857 ATTCAATGAGCTAAGGAACACTACAGGACTTCTACAAATTTTCAGTTGATGTCG 916
Db 323 ATAGAAGGACATGAGGAGACATCATATGACCACTGAGAGATTTAAGATGACGTCA 382
Qy 917 CAATAATACCATTTGATATTGCTACCTCTTCTTTGGGTTTAAATCCAAATGTTAG 976
Db 383 GCTTGTTCCTCGTGAGATATCTTATGTTTTCAGTGAGTCACTCTCTGTGAGTTCC 442
Qy 977 ATAGATGTTAAAGTACATCTTATTTTGAATTTATCATCATCAGTACGATCTATAG 1036
Db 443 CTCGGCTGCTGAAGTACATGCGGTTCTTTGAGTTTCAATGACCGGATGGAGCTG 502
Qy 1037 ACAAGCATATATCTACAGAGTTATTCGAACAACTGGATCTCTGTTTATCTGAC 1096
Db 503 AGAAGCATATCTACAGGTTGATCCGGAGCTCCAGTACCTCTCTCTCTCTGAC 562
Qy 1097 TTAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAG 1156
Db 563 TCAAGCTGTGCTCTTTTATTTGGGATCAGACTACGAGGACTCGATCCCAAGTGG 622
Qy 1157 TGTATGATGGGAGAGAAACAGATATCTGAGATGTTATTTATGGGAGTTCGAATTA 1216
Db 623 TCTACGAGGAGAAAGAAACGCTTATATCCGCTGTGTACTTTTGGGAGGACATTTGA 682
Qy 1217 TTACCATTTGGGCTTCCAGAACACAACTTTATTTGAATTTGTTTTCACCTTTGA 1276
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Qy 1277 ATTTTCTTCTGAGTTTCTGTTCTCCAGTTTAAATTTGGTCAGATGAGATGTCATTC 1336
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Qy 1337 GAGCAGTACAGCAATCAGAACTACTTCCGGGCTTCGATGATGATGACACACATTCG 1396
Db 803 GAGCTGCGACCCCGGAGAGACTACTACCGAGCTGCTGATGAGACACACATTCAGT 862
Qy 1397 TGAACAATTTACTTCCATTCCTAACTTTGTGCAAAAGGAGTTTCGGACTTGGTATGA 1456
Db 863 TGAACCTCTTTTACACATCCCCCGACAGGTCAGAACCCGATCAAGAACTGTTACG 922
Qy 1457 CATGGAGCTCTCAAGAAATGCTAGATGACTGCTGATTTGCTTAAAGACCTTACCA 1516
Db 923 CTTGGAAGATTCAGGCGCATGCTGGATGA-ACAGAGCTTCTTAGTGCAGCTCCCG 981
Qy 1517 TCCAGTTAGCTTCGCGCATTTGATGTGAACCTTCAGCATCATCAGCAAAAGTTCG 1575
Db 982 TGAGGCTGAGCTTGGCTGGAAAACACTACACTAATCCCTTCTCAGCAAAAGTGG 1041
Qy 1576 AAGGGTTGTGATACACAGA---TGATTATGACATGTTGCTAAGATTGAATTCG 1632
Db 1042 CAGGGCTGTGAAAAAATAAATGGGTTTCCACCTGTTAAACCAAGTTCCAGTCAG 1101
Qy 1633 TATTTGCTGCTGCTGCTTCTGTCAAAAAGGGAGAA 1668
Db 1102 ACCTGCCCGGAAACTTTGCTGTAAAAAGGCGAAA 1137
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RESULT 14

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BX401127
LOCUS
DEFINITION BX401127 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK009YE13 5-PRIME, mRNA sequence.
ACCESSION BX401127
VERSION BX401127.2 GI:46846684
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 1054)
Li, W.B., Gruber, C., Jesssee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 13, 2003 this sequence version replaced gi:30614460.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
7817.r
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For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?se=CS0DK009AC070Pl&c=7817.r.

FEATURES
source

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/notes="1st strand cDNA was primed with a NotI-oligo(dT)
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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ORIGIN

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QY 861 AAATGAGCTAAGAAACACTACAGGACTCTTACAAAATTTTCAGTTGGATGTCGCATCAAT 920
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Db 4 AAAGGATATCGGAAATAACTACCTGAAGTCTCGCCGCTTCAAGATGGACCTGCTCAGCCT 63

QY 921 AATACATTGTGATATTTGCTACTCTCTCTTTCGGTTTATCCAAATGTTTAGAGCAATAG 980
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Db 64 CTGCGCTTGGATTTTCTCTATTGAACTCGTGGAACCCCTCTCTCGCYVTGCMCG 123

QY 981 GATGTTAAA--GTACACTTTCATTTTTTGAATTTAATCATCACCTAGAGTCTATAATGGAC 1038
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 124 CTGTTTAAATGATCATGCGCTTCTTCGAGTTTAAACGCGGCTGGAATCCATCCTCAGC 183

QY 1039 AAAGCATATATCTACAGAGTTAATGAAACAACTGGATATCTGCTGTTTATTTCTGCACAT 1098
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Db 184 AAAGCCTACGTGTACAGGGTCTACAGAYCACAGYTTACCTTCTTTACAGCCTGCATTG 243

QY 1099 AATGCTGTGTTTATTACTGGGCTTCARACTATGAAGAAATGGCACTACTAGATGGTG 1158
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Db 244 AATTCTGTCTTATTACTTGGGATCGGCTATCAGGGCTCGGCTCCACTCACTGGGT 303

QY 1159 TATGATGGGGAAGAAACGAGTATCTGAGATGTTATTATTGGGCGAGTTCGAACCTTTAAT 1218
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Db 304 TACGATGGCGTGGGAAACAGTTATATTCGTGTACTATTGCTGTGAACMCTCATC 363

QY 1219 ACCATTGTGGGCTTCCAGAACCAAACTTTATTGAAATTTGTTTTCAACTCTTGAAT 1278
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Db 364 AYTCTGGGGGGCTGCTCAGCCCAAGAYACTCTTTGAAATTTGCTTCCAGCTGVTGAAT 423

QY 1279 TTTTTTCTCGAGTTTCTGTTCTCCAGTTTAAATGTTGTCAGATGAGATGTGATGGA 1338
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Db 424 TATTTACGGGGGCTTCTGCTTCTGTGTGATGTTGGACAGATGAGATGTGTAGGG 483

QY 1339 GCAGCTACAGCCAATCAGAACTACTTCCCGGCTGCTAGTGGATGACACCAATTCCTACATG 1398
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Db 484 GCGGCCACCG-CAGACAGACCTACTACCGCAGCTGCATGACAGCAGCAGTGAATGATG 542

QY 1399 ACAATTAATCTCATCTTAACTTTGTGAAAAGCGAGTTCCGACTTGGTATGAATATACA 1458
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QY 1459 TGGGACTCTCAAGAAATGCTAGATGAGTCTGATTTGCTTTAAGACCTCAACCACTACGGTC 1518
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Db 783 CCCAACGATATGTGTGCAGAAAGVGGGSAGATCGGCCGTGAGATGTATCATCATCGGC 842

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QY 1758 TGGGTGCGTGTGTTGAGAAATCAGCCTCTACAGCAGAGAGGAGAAACCGTCGAACTGC 1817
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QY 1818 CAATGCTGTGGCCACGGGTTTGCCAACTCTTTTAATCTCTAGACAA 1862
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DEFINITION Pan troglodytes CNGB1 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION  DQ032774
VERSION    DQ032774.1
KEYWORDS   GSS
SOURCE     Pan troglodytes (chimpanzee)
ORGANISM   Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Pan.
REFERENCE  1 (bases 1 to 3444)
            Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.R.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
            A Scan for Positively Selected Genes in the Genomes of Humans and
            Chimpanzees
            (er) PLoS Biol. 3 (6), E170 (2005)
JOURNAL    PLoS Biol. 3 (6), E170 (2005)
PUBMED     15869325
REFERENCE  2 (bases 1 to 3444)
            Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.R.,
            Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
            White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
            Direct Submision
            Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT    This sequence was made by sequencing genomic exons and ordering
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ORIGIN
Query Match      13.7%; Score 333.8; DB 11; Length 3444;
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Matches 482; Conservative 0; Mismatches 865; Indels 0; Gaps 0;

QY 617 TTCAAAACAGCATAGATTACACAGATCGACTCTATCTCTCTGTGGCTCTTTGTTGCA 676
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QY 677 CTCCTTGCCTATAACTGGAACTGCTGTTTATACCACCTCGCCTCGCTTCCCATATCAA 736
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QY 737 CGCAGACAACATACACTACTGCGCTTATTGCGGACATCATATGTATCATCTACTCTT 796
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QY 797 ATGATATGCTATTTATCCAGCCGACATCTCCAGTTGTTGAAGAGGAGACATAATAGTGG 856
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Db 2093 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2152

QY 857 ATTCAAATGACTAAGGAAACACATACAGACTCTTACAAAATTTTCAGTTGGATGTCGCAT 916
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Db 2153 ACAAAAGGACATCGGAAATAACTACTGGAATCTCGCCGCTTCAAGNNNNNNNNNNNN 2212
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QY 917 CAATAATACCAATTTGATATTTGTACTCTCTCTTTGGGTTTAAATCCAATGTTTAGACAA 976
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Db 2213 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 2272

QY 977 ATAGATGTTAAAGTACACTTCACTTTTGTGAATTTTAAATCATCATCAGCTAGAGTCTATAATGG 1036
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 17:07:01 ; Search time 446 Seconds
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Perfect score: 2430
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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	329.6	13.6	601	3	US-09-949-016-38930
6	329.6	13.6	601	3	US-09-949-016-38931
7	329.6	13.6	601	3	US-09-949-016-205286
8	329.6	13.6	601	3	US-09-949-016-205287
9	202	8.3	601	3	US-09-949-016-38898
10	202	8.3	601	3	US-09-949-016-205176
11	181.2	7.5	2796	3	US-09-949-016-5678
12	169.8	7.0	84571	3	US-09-949-016-17420
13	151.4	6.2	601	3	US-09-949-016-38897
14	151.4	6.2	601	3	US-09-949-016-205175
15	147.6	6.1	601	3	US-09-949-016-38915
16	147.6	6.1	601	3	US-09-949-016-205232
17	144.6	6.0	601	3	US-09-949-016-205228
18	144.6	6.0	601	3	US-09-949-016-205229
19	143	5.9	601	3	US-09-949-016-38929
20	143	5.9	601	3	US-09-949-016-205285
21	132.8	5.5	3470	3	US-09-949-016-4344
22	132.8	5.5	32665	3	US-09-949-016-16086
23	102.6	4.2	601	3	US-09-949-016-38918
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C 26	91.4	3.8	601	3	US-09-949-016-38908	Sequence 38908, A
C 27	91.4	3.8	601	3	US-09-949-016-205201	Sequence 205201, A
C 28	87	3.6	996	3	US-09-270-767-15059	Sequence 15059, A
29	85.6	3.5	2223	2	US-08-257-073-4	Sequence 4, Appl
30	79	3.3	1728	3	US-09-927-267-3	Sequence 3, Appl
31	79	3.3	2308	3	US-09-927-267-2	Sequence 2, Appl
32	79	3.3	2366	3	US-09-799-451-351	Sequence 351, App
C 33	78.8	3.2	929	3	US-09-671-317-14	Sequence 14, Appl
C 34	78	3.2	64309	3	US-09-949-016-14581	Sequence 14581, A
C 35	73.6	3.0	444	3	US-09-270-767-11944	Sequence 11944, A
C 36	73.6	3.0	7044	3	US-09-949-016-14113	Sequence 14113, A
C 37	72.8	3.0	1001	3	US-09-671-317-439	Sequence 439, App
C 38	72.6	3.0	1282	3	US-10-002-344A-89	Sequence 89, Appl
C 39	71	2.9	601	3	US-09-949-016-38919	Sequence 38919, A
C 40	71	2.9	601	3	US-09-949-016-205248	Sequence 205248, A
C 41	70	2.9	88002	3	US-09-949-002-639	Sequence 639, App
C 42	70	2.9	88002	3	US-09-949-002-717	Sequence 717, App
C 43	68.2	2.8	3117	3	US-09-614-221A-275	Sequence 275, App
C 44	67.8	2.8	4167	3	US-09-973-278-700	Sequence 700, App
C 45	66.8	2.7	612	3	US-09-902-540-1357	Sequence 1357, Ap

ALIGNMENTS

RESULT 1
US-09-949-016-1074
; Sequence 1074, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1074
; LENGTH: 2135
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-1074

Query Match	84.3%	Score	2049.4	DB 3	Length	2135
Best Local Similarity	99.2%	Pred. No. 0				
Matches	2075	Conservative	0	Mismatches	1	Gaps 1
Qy	340	CCACAAACAAACCGCTGCTGTTTATTAATAGTATGCCGATGCCAGCTACAC	399			
Db	1	CCACAAACAAACCGCTGCTGTTTATTAATAGTATGCCGATGCCAGCTACAC	60			
Qy	400	AACCTGGTGAAGAATGGTCAAGAACAGCCCTCTACAAGAAAGTTGGTAGAGGA	459			
Db	61	AACCTGGTGAAGAATGGTCAAGAACAGCCCTCTACAAGAAAGTTGGTAGAGGA	120			
Qy	460	GATCTCTCTCCACCGAAGCCAGCCACAACTGCAAGCCCGCTGTACCAACAGTA	519			
Db	121	GATCTCTCTCCACCGAAGCCAGCCACAACTGCAAGCCCGCTGTACCAACAGTA	180			
Qy	520	AAAGAAAGCGATGAAGCAACAGAACTATTAACAGGCTGTGTGTTTCAAGTCAA	579			
Db	181	AAAGAAAGCGATGAAGCAACAGAACTATTAACAGGCTGTGTGTTTCAAGTCAA	240			
Qy	580	AAGATGCTTTACAGAGTACTTAAAGCGAATTAACCTTCAACACAGCATAGTTAC	639			

Db 241 AAGATGCCCTTTAAACAGAGTACTTAAAGCGAATTAATACTTCCAAAACAGCATAGATTTCATAC 300
Qy 640 ACAGATCGACTCTATCTCTGTGGCTCTTGCCTTGTCACTCTTGCCTATATAACTGGAACTGC 699
Db 301 ACAGATCGACTCTATCTCTGTGGCTCTTGTGTCACTCTTGCCTATATAACTGGAACTGC 360
Qy 700 TGGTTTATACCACTGGCCCTGCTTCCCATATCAAAACCGCAGACAACATACACTACTGG 759
Db 361 TGTTTTATACCACTGGCCCTGCTTCCCATATCAAAACCGCAGACAACATACACTACTGG 420
Qy 760 CTTATTGGCGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCC 819
Db 421 CTTATTGGCGACATCATATGTGATATCATCTACCTTTATGATATGCTATTTATCCAGCCC 480
Qy 820 AGACTCCAGTTTGAAGAGGAGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACAC 879
Db 481 AGACTCCAGTTTGAAGAGGAGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACAC 540
Qy 880 TACAGACTTCTACAAAATTTGAGTTGGATGCGCATCAATATACCATTTGATATTGC 939
Db 541 TACAGACTTCTACAAAATTTGAGTTGGATGCGCATCAATATACCATTTGATATTGC 600
Qy 940 TACCTCTCTTTGGGTTTAAATCCAATGTTTAGAGCAATAGGATGTTAAGTACACTTCA 999
Db 601 TACCTCTCTTTGGGTTTAAATCCAATGTTTAGAGCAATAGGATGTTAAGTACACTTCA 660
Qy 1000 TTTTGTGAATTTAATCATCACCTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTT 1059
Db 661 TTTTGTGAATTTAATCATCACCTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTT 720
Qy 1060 ATTGCAACAACCTGGATCTGCTGTTTATTTCGCACATTAATGCCCTGTGTTTACTGG 1119
Db 721 ATTGCAACAACCTGGATCTGCTGTTTATTTCGCACATTAATGCCCTGTGTTTACTGG 780
Qy 1120 GCTTCAAACTATGAGGAATTTGGCACTACTAGATGGTGTATGATGGGGAAGAAACGAG 1179
Db 781 GCTTCAAACTATGAGGAATTTGGCACTACTAGATGGTGTATGATGGGGAAGAAACGAG 840
Qy 1180 TATCTGAGATGTTATTATTGGGAGTTTCGAACCTTTAATTAACCATTTGGTGGCCTTCAGAA 1239
Db 841 TATCTGAGATGTTATTATTGGGAGTTTCGAACCTTTAATTAACCATTTGGTGGCCTTCAGAA 900
Qy 1240 CCACAACTTTATTGAAATTTGTTTCAACTCTGAAATTTTCTGGAGTTTGTG 1299
Db 901 CCACAACTTTATTGAAATTTGTTTCAACTCTGAAATTTTCTGGAGTTTGTG 960
Qy 1300 TTCTCCAGTTTAAATGGTCCAGATGAGATGTGATTGGAGCAGCTACAGCCCAATCAGAAC 1359
Db 961 TTCTCCAGTTTAAATGGTCCAGATGAGATGTGATTGGAGCAGCTACAGCCCAATCAGAAC 1020
Qy 1360 TACTTCCGCGCTGATGGATGACACCAATGCGCTACATGAACAATTTACTTCCATTTCTTAAA 1419
Db 1021 TACTTCCGCGCTGATGGATGACACCAATGCGCTACATGAACAATTTACTTCCATTTCTTAAA 1080
Qy 1420 CTTGTGCAAAAACGGAGTTCCGACTTGGTATGAATATACATGGGACTCTCAAAAGATGCTA 1479
Db 1081 CTTGTGCAAAAACGGAGTTCCGACTTGGTATGAATATACATGGGACTCTCAAAAGATGCTA 1140
Qy 1480 GATGAGTCTGATTTGCTTAAAGACCTTACCACCTAGGTCAGCTAGCCCTCGCCATTGAT 1539
Db 1141 GATGAGTCTGATTTGCTTAAAGACCTTACCACCTAGGTCAGCTAGCCCTCGCCATTGAT 1200
Qy 1540 GTGAATCTCAGCATCATCAGCAAAAGTCGACTTGTTCGAGGGTGTGATACACAGATGATT 1599
Db 1201 GTGAATCTCAGCATCATCAGCAAAAGTCGACTTGTTCGAGGGTGTGATACACAGATGATT 1260
Qy 1600 TATGACATGTTCTTAAGATTGAAATCCGTTCTCTATTTCGCTGGTGAATTTGCTGCAAA 1659
Db 1261 TATGACATGTTCTTAAGATTGAAATCCGTTCTCTATTTCGCTGGTGAATTTGCTGCAAA 1320
Qy 1660 AAGGAGAAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAAAGTCCAAAGTCTTGGAA 1719
Db 1321 AAGGAGAAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAAAGTCCAAAGTCTTGGAA 1380

Qy 1720 GGCCCTGATGGTACTAAAGTTCTGTGTTACTCTGAAAGCTGGGTGGTGTTCGAGAAATTC 1779
Db 1381 GGCCCTGATGGTACTAAAGTTCTGTGTTACTCTGAAAGCTGGGTGGT --- 1427
Qy 1780 AGCCTTCTAGCAGCAGGAGGAGAAACCGTGGAACTGCAATGTGGTGGCCCCACGGGTTT 1839
Db 1428 --CCTTCTAGCAGCAGGAGGAGAAACCGTGGAACTGCAATGTGGTGGCCCCACGGGTTT 1485
Qy 1840 GCCAATCTTTTAACTCTAGACAAAGAACCCCTCCAAAGAAATTTCTAGTGCATTTCCAGAT 1899
Db 1486 GCCAATCTTTTAACTCTAGACAAAGAACCCCTCCAAAGAAATTTCTAGTGCATTTCCAGAT 1545
Qy 1900 TCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGCTTAAGACCCGA 1959
Db 1546 TCTGAAAGGATCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAAGCTTAAGACCCGA 1605
Qy 1960 GAAGCAACCCCTCCAAAGAAAGATCTTGCCTCTCTTCCCAACCCGAAAGAGACACCC 2019
Db 1606 GAAGCAACCCCTCCAAAGAAAGATCTTGCCTCTCTTCCCAACCCGAAAGAGACACCC 1665
Qy 2020 AAACCTGTTTAAACCTCTCTAGGAGGCACAGAAAGCAAGTCTTTCGAAGACTACTCAA 2079
Db 1666 AAACCTGTTTAAACCTCTCTAGGAGGCACAGAAAGCAAGTCTTTCGAAGACTACTCAA 1725
Qy 2080 TTGAAGCGAGAGCAAGCAGCTCAGAAAGAAAGAAATTTCTGAAGGAGGAGGAAAGGA 2139
Db 1726 TTGAAGCGAGAGCAAGCAGCTCAGAAAGAAAGAAATTTCTGAAGGAGGAGGAAAGGA 1785
Qy 2140 AAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGATAA 2199
Db 1786 AAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGAAATGAAGATAAACAAGATAA 1845
Qy 2200 GGAAAGAAAGAAATGAAGATAAAGATAAAGAGAGCCAGAGAGGAGGAGGAGGAGGAGG 2259
Db 1846 GGAAAGAAAGAAATGAAGATAAAGATAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1905
Qy 2260 CCTGAATGTACAGCAAGTCTTATTCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2319
Db 1906 CCTGAATGTACAGCAAGTCTTATTCAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1965
Qy 2320 GTTTTACCAGAGGAGCTTCTGCTCAATCACTCATTATCAGATGGCTCTTCTCTCTGAG 2379
Db 1966 GTTTTACCAGAGGAGCTTCTGCTCAATCACTCATTATCAGATGGCTCTTCTCTCTGAG 2025
Qy 2380 GSCGAGAGAGAGTCTTACTATTGAAGTCAAGAAAGGCTTAAGCAATAA 2430
Db 2026 GSCGAGAGAGAGTCTTACTATTGAAGTCAAGAAAGGCTTAAGCAATAA 2076

RESULT 2

US-09-949-016-5798
; Sequence 5798, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE OF INVENTION: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5798
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-5798

Query Match	83.8%	Score	2035.4	DB 3	Length	2139			
Best Local Similarity	99.0%	Pred. No.	0						
Matches	2075	Conservative	0	Mismatches	1	Indels	19	Gaps	2
Qy	340	CCACAAACAAACCGCTCGAGCTCCTCTGTTATATAATGAGTATGCCGATGCCAGCTACAC	399						
Db	1	CCACAAACAAACCGCTCGAGCTCCTCTGTTATATAATGAGTATGCCGATGCCAGCTACAC	60						
Qy	400	AACCTGGTGAAGAAGTGCCTCAAGAACAGCCCTCTCAAGAAAAAGTTGGTAGAGGA	459						
Db	61	AACCTGGTGAAGAAGTGCCTCAAGAACAGCCCTCTCAAGAAAAAGTTGGTAGAGGA	120						
Qy	460	GATCTCTCTCACCCGAAGCCAGCCCAACATGCAAGCCACCGCTGTACCAACAGTA	519						
Db	121	GATCTCTCTCACCCGAAGCCAGCCCAACATGCAAGCCACCGCTGTACCAACAGTA	180						
Qy	520	AAAGAAAGCGATGATAAGCCCAACAGAACATTACTACAGGCTGTGTGGTTCAAAGTCAAA	579						
Db	181	AAAGAAAGCGATGATAAGCCCAACAGAACATTACTACAGGCTGTGTGGTTCAAAGTCAAA	240						
Qy	580	AAGATGCTTTAAACAGAGTACTTAAAGCGAATTAACCTCCAAACAGCATAGATTCTATC	639						
Db	241	AAGATGCTTTAAACAGAGTACTTAAAGCGAATTAACCTCCAAACAGCATAGATTCTATC	300						
Qy	640	ACAGATCGACTCTATCTCCTGTGGCTCTTGCTGTCTACTCTTGCTATAACTGGAAGTGC	699						
Db	301	ACAGATCGACTCTATCTCCTGTGGCTCTTGCTGTCTACTCTTGCTATAACTGGAAGTGC	360						
Qy	700	TGGTTTATACCACTCGCGCTCGTCTCCATATCAAAACCGAGAGCAACATCACTACTGG	759						
Db	361	TGGTTTATACCACTCGCGCTCGTCTCCATATCAAAACCGAGAGCAACATCACTACTGG	420						
Qy	760	CTTATTCGGACATCATATGTGATATCATCTACCTCTTATGATATGCTATTTATCCAGCCC	819						
Db	421	CTTATTCGGACATCATATGTGATATCATCTACCTCTTATGATATGCTATTTATCCAGCCC	480						
Qy	820	AGACTCCAAGTTTGAAGAGGAGGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACAC	879						
Db	481	AGACTCCAAGTTTGAAGAGGAGGAGACATAATAGTGGATTCAAAATGAGCTAAGGAAACAC	540						
Qy	880	TACAGGACTTCTCAAAAATTTTCAGTTGGATGTCGCATCAATAATACCAATTTGATATTTC	939						
Db	541	TACAGGACTTCTCAAAAATTTTCAGTTGGATGTCGCATCAATAATACCAATTTGATATTTC	600						
Qy	940	TACCTCTCTTTGGGTTTAAATCCAAATGTTAGAGCAAAATAGAGTGTAAAGTACACTTCA	999						
Db	601	TACCTCTCTTTGGGTTTAAATCCAAATGTTAGAGCAAAATAGAGTGTAAAGTACACTTCA	660						
Qy	1000	TTTTTTGAAATTTAATCATCACTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTT	1059						
Db	661	TTTTTTGAAATTTAATCATCACTAGAGTCTATAATGGACAAAGCATATATCTACAGAGTT	720						
Qy	1060	ATTCGAAACAATGGATACCTGCTGTTTATCTCGACATTAATGCTGTGTTTATTACTGG	1119						
Db	721	ATTCGAAACAATGGATACCTGCTGTTTATCTCGACATTAATGCTGTGTTTATTACTGG	780						
Qy	1120	GCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTGTATGATGGGAAAGGAAACGAG	1179						
Db	781	GCTTCAAACTATGAAGAAATGGCACTACTAGATGGGTGTATGATGGGAAAGGAAACGAG	840						
Qy	1180	TATCTGAGATGTTATTTATTTGGCAGTTCGAACCTTTAATACCATTTGGTGGCTTCCAGAA	1239						
Db	841	TATCTGAGATGTTATTTATTTGGCAGTTCGAACCTTTAATACCATTTGGTGGCTTCCAGAA	900						
Qy	1240	CCACAAACTTTATTTGAAATGTTTTTCAACTCTGAAATTTTTTTCTGGAGTTTTTTGTG	1299						
Db	901	CCACAAACTTTATTTGAAATGTTTTTCAACTCTGAAATTTTTTTCTGGAGTTTTTTGTG	960						
Qy	1300	TTCTCCAGTTTTAAATTTGGTCAGATGAGATGTGATTTGAGCAGCTTACAGCCAATCAGAAC	1359						
Db	961	TTCTCCAGTTTTAAATTTGGTCAGATGAGATGTGATTTGAGCAGCTTACAGCCAATCAGAAC	1020						

Qy	1360	TACTTCGGCGCCTGCATGATGACACCAATTGCCATAGTAAACAATTTACTTCCATCTCTCTAAA	1411
Db	1021	TACTTCGGCGCCTGCATGATGACACCAATTGCCATAGTAAACAATTTACTTCCATCTCTCTAAA	1080
Qy	1420	CTTGTCCAAAGCGAGTTCGGACTTGGTATGAATAFACATGGGACTCTCAAAGAATGCTTA	1479
Db	1081	CTTGTCCAAAGCGAGTTCGGACTTGGTATGAATAFACATGGGACTCTCAAAGAATGCTTA	1140
Qy	1480	GATGAGTCTGATTTGCTTTAAGACCCTACCAACTACGGTCCAGTTAGCCCTTCGCCATTGAT	1539
Db	1141	GATGAGTCTGATTTGCTTTAAGACCCTACCAACTACGGTCCAGTTAGCCCTTCGCCATTGAT	1200
Qy	1540	GTGAACCTTCAGCATCATCAGCAAAAGTCGACTTGTTCGAAG-----GGTTGTGATACACAGAT	1595
Db	1201	GTGAACCTTCAGCATCATCAGCAAAAGTCGACTTGTTCGAAGCCAAGGTTGTGATACACAGAT	1260
Qy	1596	GATTTATGACATCTGCTTAAGATTGAAATCCGGTTCTATTTCGCTGGTGACTTTGTCTG	1655
Db	1261	GATTTATGACATCTGCTTAAGATTGAAATCCGGTTCTATTTCGCTGGTGACTTTGTCTG	1320
Qy	1656	CAAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGGAGAAAGTCCAAAGTTCT	1715
Db	1321	CAAAAAAGGAGAAATTTGGCAAGGAAATGTATATCATCAAGCATGGAGAAAGTCCAAAGTTCT	1380
Qy	1716	TGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAGCTGGGTGCGTGTTCGGAGA	1775
Db	1381	TGGAGGCCCTGATGGTACTAAAGTTCTGGTTACTCTGAAAGCTGGGTGCGTGTTCGGAGA	1431
Qy	1776	AATCAGCCTCTTAGCAGCAGGAGGAGGAAACCGTCGAACTGCCAAATCTGGTGCCCCACAGG	1835
Db	1432	-----CCTTCTTAGCAGCAGGAGGAGGAAACCGTCGAACTGCCAAATCTGGTGCCCCACAGG	1485
Qy	1836	GTTTGCCAACTTTTTAACTCTAGACAAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTTATCC	1895
Db	1486	GTTTGCCAACTTTTTAACTCTAGACAAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTTATCC	1545
Qy	1896	AGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTCTTTTTAAAGCAGAAAGCTTAAGAC	1955
Db	1546	AGATTCTGAAAGGATCCTCATGAAGAAAGCCAGAGTCTTTTTAAAGCAGAAAGCTTAAGAC	1605
Qy	1956	CGCAGAAAGCAACCCCTCCAAGAAAGATCTTGGCCTCTCTTCCCACCCGAAAGNAGAGAC	2015
Db	1606	CGCAGAAAGCAACCCCTCCAAGAAAGATCTTGGCCTCTCTTCCCACCCGAAAGNAGAGAC	1665
Qy	2016	ACCCAAACTGTTTAAACTCTCTTAGSAGCACAGGAAAGCAAGTCTTCCAAAGACTACT	2075
Db	1666	ACCCAAACTGTTTAAACTCTCTTAGSAGCACAGGAAAGCAAGTCTTCCAAAGACTACT	1725
Qy	2076	CAAAATTGAAGCGAGCAGCAAGCAGCTCAGAGAAAGAAAAATTTCTGAAGGAGGAGGAAGA	2135
Db	1726	CAAAATTGAAGCGAGCAGCAAGCAGCTCAGAGAAAGAAAAATTTCTGAAGGAGGAGGAAGA	1785
Qy	2136	AGGAAAAAGAAAATGAAGATTAACAAAAAGAAAAATGAAGATTAACAAAAAGAAAAATGAAGA	2195
Db	1786	AGGAAAAAGAAAATGAAGATTAACAAAAAGAAAAATGAAGATTAACAAAAAGAAAAATGAAGA	1845
Qy	2196	TAAAGGAAAGAAAAATGAAGATAAGATAAGGAGAGAGCCAGNAGAGCCACTTGGGA	2255
Db	1846	TAAAGGAAAGAAAAATGAAGATAAGATAAGGAGAGAGCCAGNAGAGCCACTTGGGA	1905
Qy	2256	CAGACCTGAAATGTACAGCAAGTCTCTATTGAGTGGAGGAAAGAACCCCACTCAGTTAGAAG	2315
Db	1906	CAGACCTGAAATGTACAGCAAGTCTCTATTGAGTGGAGGAAAGAACCCCACTCAGTTAGAAG	1965
Qy	2316	GACAGTTTTTACCCAGAGGACTTCTCGTCAATCACTATTATCAGCATGCGTCTCTCTGCG	2375
Db	1966	GACAGTTTTTACCCAGAGGACTTCTCGTCAATCACTATTATCAGCATGCGTCTCTCTGCG	2025
Qy	2376	TGAGGGCGGAGAAAGGTTTCTTACTATTGAAGTCAAAAGAAAGGCTTAAGCAATAA	2430
Db	2026	TGAGGGCGGAGAAAGGTTTCTTACTATTGAAGTCAAAAGAAAGGCTTAAGCAATAA	2080

[illegible]

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QY 1130 ATGAAGGATTTGGCACTACTAGATGGGTGA-----TGATG 1165
Db 11062 CTAATGGATTTGGAAATGATACATAGGCTCTACCCCTGATATTAATGATCCTGAATTTGGCC 81121
QY 1166 GCGAAGGAAACAGATCTGAGATGTTATTTATTTGGGCAAGTTCGAACCTTTAAATTTACCATTTG 1225
Db 81122 GTTTGGCTAGAAATACGTATACAGCCTTTACTGGTCTACATGACTTTTGACTACCATTTG 81181
QY 1226 GTGGCCTTCCGAAACCAAACTTTATTTGAAATTTGTTTTTCAACTCTTTGAATTTTTTTTT 1285
Db 81182 GTGAAACACCCCTCCCGTGAGGATTCAGATGATGCTTTGTGGTGGTTGATTTCTCTAA 81241
QY 1286 CTGGAGTTTTTTGTGTTCTCCAGTTTAATTTGGTCAGATGAGAGATGATTTGAGCAGCTA 1345
Db 81242 TTGGAGTGTTAAATTTTGTACCATCGTTGGTAACATAGGTTCTATGATTTTCCAAACATGA 81301
QY 1346 CAGCCAAATCAGAACTACTTTCGCGCTGATGATGATGACACCAATGCTCATACAACTT 1405
Db 81302 ATGCAGCCAGACGAAATTTCAAGCAAGAAATGATGCTATCAAGCAATATATGCAATTTTC 81361
QY 1406 ACTCCATTCCTAAACTTTGTGCAAAAGCGAGTTGCGACTTTGGTATGAAATATACATGGGACT 1465
Db 81362 GAAATGTAAGCAAGATATATGGAAGAGAGGTTATTAATGTTTGTACTACCTGTGGACCA 81421
QY 1466 CTCGAAGATGCTAGATGATCTGATTTGCTTTAAGACCCCTACCAACTACGGTCCAGTTAG 1525
Db 81422 ACAAATAAAACAGTTGATGAGAAAGAGTCTTAAAGTATCTACCTGATATAAATAAGAGCAG 81481
QY 1526 CCTCGCCATGATGTGAATCTTCAGCATCATCAGCAAAAGTCGACTTTGTTCAAGGGTTTG 1585
Db 81482 AAATTGCCATCAACGTTTCACTTAGACACATTAATAAAGGTACGCATTTTGTGCTGATTTG 81541
QY 1586 ATACACAGATGATTTATGACATGTTGCTAAGATTTGAAATCCGTTCTCTATTTTGCCTGGTG 1645
Db 81542 AAGCTGCTGTTTGGTGGAGTTGGTCTTGAAATGCAACCCCAAGTCTACAGTCTCTGGAG 81601
QY 1646 ACTTTGCTGCAAAAGGAGAAATTTGGCAAGAAATGATATATCATCAAGCATGGAGAAG 1705
Db 81602 ATTATATTTTGAAGAAAGGGGATATCGGACGAGAGATGTACATTAATCAAGGAAGGCAAC 81661
QY 1706 TCCAGTTCTTGAGGCCCTGATGTTGCTAAAGTTCTCTGTT---TACTCTGAAGCTGGG 1761
Db 81662 TGCTGTGTCGACAGATGATGAGTCACTCAGTTTGTGTTATTTAGCGATGGCAGTACT 81721
QY 1762 TCGGTGTTTGGAGAAATC--AGCCTTCTAGCAGCAGGAGGAGAAACCGTCGAACTGCCA 1819
Db 81722 TCGGTGAGATCAGCATTTCTTAACATTTAAAGGAGCAAAAGCTGCAATCGAAGAACGGCCA 81781
QY 1820 ATGTGTGTCGCCACGGGTTTGCCAATCTTTTAACCTAGACAAAGAACCCCTCCAGAA 1879
Db 81782 ATATTAAAGATATTGGCTACTCAGACCTGTTCTGTCTCTCAAAAGATGACCTCATGGAAG 81841
QY 1880 TTCTAGTCATTTATCCAGATTTCTGAAGGATCTCATGAAGAAAGCCAGAGTCTTTTAA 1939
Db 81842 CTCTAACTAGTACCCAGATGCAAACTATGCTGGAAGAAAGGGAAGCAGATTTTAA 81901
QY 1940 ACAGAAGGCT 1950
Db 81902 TGAAGATGGT 81912
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RESULT 13
US-09-949-016-38897/c
; Sequence 38897, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38897
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38897
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Query Match 6.2%; Score 151.4; DB 3; Length 601;
Best Local Similarity 99.3%; Pred. No. 2.3e-27;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 493 GCAAGCCACGGCTGTACCCAGTAAAGAAAGCGATGATAAGCCAAACGAACTTAC 552
Db 291 GCAAGCCACGGCTGTACCCAGTAAAGAAAGCGATGATAAGCCAAACGAACTTAC 232
QY 553 TACAGGCTGTTGTGTTCAAAAGTCAAAAGATGCTTTTAAACAGAGTACTTTAAAGCGAATT 612
Db 231 TACAGGCTGTTGTGTTCAAAAGTCAAAAGATGCTTTTAAACAGAGTACTTTAAAGCGAATT 172
QY 613 AAACCTTCCAAACAGCATAGATTCATACACAGAT 645
Db 171 AAACCTTCCAAACAGCATAGATTCATACACAGAT 139
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RESULT 14
US-09-949-016-205175/c
; Sequence 205175, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205175
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-205175
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Query Match 6.2%; Score 151.4; DB 3; Length 601;
Best Local Similarity 99.3%; Pred. No. 2.3e-27;
Matches 152; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 493 GCAAGCCACGGCTGTACCCAGTAAAGAAAGCGATGATAAGCCAAACGAACTTAC 552
Db 291 GCAAGCCACGGCTGTACCCAGTAAAGAAAGCGATGATAAGCCAAACGAACTTAC 232
QY 553 TACAGGCTGTTGTGTTCAAAAGTCAAAAGATGCTTTTAAACAGAGTACTTTAAAGCGAATT 612
Db 231 TACAGGCTGTTGTGTTCAAAAGTCAAAAGATGCTTTTAAACAGAGTACTTTAAAGCGAATT 172
QY 613 AAACCTTCCAAACAGCATAGATTCATACACAGAT 645
Db 171 AAACCTTCCAAACAGCATAGATTCATACACAGAT 139

RESULT 15
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US-09-949-016-38915/c
; Sequence 38915, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38915
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-38915

Query Match 6.1%; Score 147.6; DB 3; Length 601;
Best Local Similarity 97.4%; Pred. No. 2e-26;
Matches 150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 601 GGAGCAGCTACAGCAATCAGAACTACTTCGGCGCCTGCGATGATGACACCATTTGCCTAC 542
QY 1396 ATGAACAATTACTCCATTCCTAACTTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATAT 1455
Db 541 ATGAACAATTACTCCATTCCTAACTTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATAT 482
QY 1456 ACATGGGACTCTCAAGAATGCTAGATGAGTCTG 1489
Db 481 ACATGGGACTCTCAAGAATGCTAGGTAAGCATG 448

Search completed: December 23, 2005, 23:22:17
Job time : 451 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 17:11:54 ; Search time 1732 Seconds
(without alignments)
11601.956 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.Main:
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10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2430	100.0	2703	3	US-09-855-828-2
3	2430	100.0	2757	3	US-09-855-828-16
4	1316	54.2	1400	10	US-11-060-756-2833
5	1316	54.2	1400	10	US-11-060-756-7105
6	654.4	26.9	2516	9	US-10-450-763-5457
7	577.4	23.8	2607	6	US-10-189-507-3
8	577.4	23.8	4382	6	US-10-159-563-147
9	573.6	23.6	3811	9	US-10-450-763-27462
10	518	21.3	2244	9	US-10-450-763-11960
11	518	21.3	2244	9	US-10-450-763-11988
12	306	12.6	680	5	US-10-027-632-204539
13	306	12.6	680	6	US-10-027-632-204539
14	223	9.2	3275	10	US-11-097-143-26426
15	176.4	7.3	2500	6	US-10-172-118-427
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17	165	6.8	581	4	US-09-925-065A-485501
18	160.6	6.6	289	9	US-10-450-763-11095
19	160	6.6	563	4	US-09-925-065A-284517
20	160	6.6	1127	4	US-09-925-065A-284516
21	136.2	5.6	2109	10	US-11-097-143-24368
22	133.2	5.5	3027	6	US-10-295-573-1
23	132.8	5.5	2085	6	US-10-345-680-27

24	132.8	5.5	3486	6	US-10-345-680-25	Sequence 25, Appli
25	131.6	5.4	1995	5	US-10-087-217-1	Sequence 1, Appli
26	131.6	5.4	1995	5	US-10-087-217-5	Sequence 5, Appli
27	131.6	5.4	1995	9	US-10-978-282-1	Sequence 1, Appli
28	131.6	5.4	1995	9	US-10-978-282-5	Sequence 5, Appli
29	131.6	5.4	3027	6	US-10-295-573-2	Sequence 2, Appli
30	131.6	5.4	3027	6	US-10-295-573-4	Sequence 4, Appli
31	129	5.3	526	3	US-09-864-761-12975	Sequence 12975, A
32	128.4	5.3	1995	5	US-10-087-217-3	Sequence 3, Appli
33	128.4	5.3	1995	5	US-10-087-217-7	Sequence 7, Appli
34	128.4	5.3	1995	9	US-10-978-282-3	Sequence 3, Appli
35	128.4	5.3	1995	9	US-10-978-282-7	Sequence 7, Appli
36	128	5.3	2877	6	US-10-295-573-3	Sequence 3, Appli
37	127	5.2	127	3	US-09-864-761-29538	Sequence 29538, A
38	124.4	5.1	5133	10	US-11-097-143-19637	Sequence 19637, A
c	120.6	5.0	5692	10	US-11-097-143-26425	Sequence 26425, A
40	111.2	4.6	1995	3	US-09-735-927-1	Sequence 1, Appli
41	111.2	4.6	1995	5	US-10-034-843-1	Sequence 1, Appli
42	111.2	4.6	1995	6	US-10-168-651-34	Sequence 34, Appli
43	111.2	4.6	1995	6	US-10-189-507-1	Sequence 1, Appli
44	111.2	4.6	2111	6	US-10-114-153-17	Sequence 17, Appli
45	111.2	4.6	2190	5	US-10-029-677-23	Sequence 23, Appli

ALIGNMENTS

RESULT 1
US-09-855-828-3
; Sequence 3, Application US/09855828
; Publication No. US20040137433A1
; GENERAL INFORMATION:
; APPLICANT: Cretech, Christopher D.
; APPLICANT: Jegla, Timothy J.
; APPLICANT: ICAGEN, Inc.
; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; FILE REFERENCE: 018512-006010US
; CURRENT APPLICATION NUMBER: US/09/855, 828
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 2000-05-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2430
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human CNG3B coding sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2430)
; OTHER INFORMATION: CNG3B
US-09-855-828-3

Query Match 100.0%; Score 2430; DB 3; Length 2430;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGTTTAAATCGGTGACAAAAGTCAACAAGTCAAGGCTATAGAGAGAAACAATGAGAAT	60
Db	1	ATGTTTAAATCGGTGACAAAAGTCAACAAGTCAAGGCTATAGAGAGAAACAATGAGAAT	60
Qy	61	GAACAAAGTTCTCGTCGGAATGAAGAGGCTCTCACCAAGTAATCAAGTCTCAGCAAAACC	120
Db	61	GAACAAAGTTCTCGTCGGAATGAAGAGGCTCTCACCAAGTAATCAAGTCTCAGCAAAACC	120
Qy	121	ACAGCACAG	180
Db	121	ACAGCACAG	180
Qy	181	ACGTCTGAAGAGCCAC	240

QY	2401	ATTGAAGTCAAGAAAGGCTAAGCAATAA	2430	541	ACAGAACATTACTACAGCGCTGTGTGGTTCAAAGTCAAAAGATGCCTTTAAACAGATAC	600
Db	2401	ATTGAAGTCAAGAAAGGCTAAGCAATAA	2430	603	ACAGAACATTACTACAGCGCTGTGTGGTTCAAAGTCAAAAGATGCCTTTAAACAGATAC	662
QY				601	TTAAAGCGAAATTAACCTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTCG	660
Db				663	TTAAAGCGAAATTAACCTTCCAAACAGCATAGATTATACACAGATCGACTCTATCTCTCG	722
QY				661	TGGCTCTTGTGTGTCACCTCTTGCCTTAACTTGAAGTCTGTGGTTTATACCACTCGCCCTC	720
Db				723	TGGCTCTTGTGTGTCACCTCTTGCCTTAACTTGAAGTCTGTGGTTTATACCACTCGCCCTC	782
QY				721	GTCTTCCCATATCAAAACCGCAGACAACATACACTACTTGGCTTATTTGCGGACATCATATGT	780
Db				783	GTCTTCCCATATCAAAACCGCAGACAACATACACTACTTGGCTTATTTGCGGACATCATATGT	842
QY				781	GATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGGA	840
Db				843	GATATCATCTACCTTTATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAGAGGA	902
QY				841	GGAGACATATAGTGGATTCAATGAGCTAAGGAACACTACAGGACTTCTACAAAATTT	900
Db				903	GGAGACATATAGTGGATTCAATGAGCTAAGGAACACTACAGGACTTCTACAAAATTT	962
QY				901	CAGTTGGATGTCGCATCAATAATACCATTTGATATTTGCTACTCTCTTTGGGTTTAAAT	960
Db				963	CAGTTGGATGTCGCATCAATAATACCATTTGATATTTGCTACTCTCTTTGGGTTTAAAT	1022
QY				961	CCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTTCAATTTTGAATTTAATCATCAC	1020
Db				1023	CCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTTCAATTTTGAATTTAATCATCAC	1082
QY				1021	CTAGAGTCTATTAATGGACAAAGCATATATCTACAGAGTTATTCGAACAACATGGATCTTG	1080
Db				1083	CTAGAGTCTATTAATGGACAAAGCATATATCTACAGAGTTATTCGAACAACATGGATCTTG	1142
QY				1081	CTGTTTATCTGCACATTAATGCCTGTGTTTATTTACTGGCTTCAAACTATGAAGGAAT	1140
Db				1143	CTGTTTATCTGCACATTAATGCCTGTGTTTATTTACTGGCTTCAAACTATGAAGGAAT	1202
QY				1141	GGCAGTCTAGATGGGTGATGATGGGGAAGGAACGAGTATCTGAGATGTTATTAATGG	1200
Db				1203	GGCAGTCTAGATGGGTGATGATGGGGAAGGAACGAGTATCTGAGATGTTATTAATGG	1262
QY				1201	GCAGTTGGAACCTTTAATTAATCCATTTGGTGGCTTTCAGAACCAACAACTTTATTTGAAAT	1260
Db				1263	GCAGTTGGAACCTTTAATTAATCCATTTGGTGGCTTTCAGAACCAACAACTTTATTTGAAAT	1322
QY				1261	GTCTTCAACTCTTGAATTTTCTGGAGTTTCTGTTCTTCTCCAGTTTAAATTTGGTCAG	1320
Db				1323	GTCTTCAACTCTTGAATTTTCTGGAGTTTCTGTTCTTCTCCAGTTTAAATTTGGTCAG	1382
QY				1321	ATGAGAGATGATGATGGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTCGCATGGAT	1380
Db				1383	ATGAGAGATGATGATGGAGCAGCTACAGCAATCAGAACTACTTCCGCGCTCGCATGGAT	1442
QY				1381	GACACCATTCCTTACATGAACAAATTAATCTCAATTCCTTAACTTTGTGTCGAAAGCGAGTTGG	1440
Db				1443	GACACCATTCCTTACATGAACAAATTAATCTCAATTCCTTAACTTTGTGTCGAAAGCGAGTTGG	1502
QY				1441	ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATCAGTCTGATTTGCTTTAAG	1500
Db				1503	ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATCAGTCTGATTTGCTTTAAG	1562
QY				1501	ACCTTACCAACTACGGTCCAGTTTGGCCCTCGCCATTTGATGTGAATTTTCCAGCATCATCAGC	1560
Db				1563	ACCTTACCAACTACGGTCCAGTTTGGCCCTCGCCATTTGATGTGAATTTTCCAGCATCATCAGC	1622
QY				1561	AAAGTCCAGTTTGAAGGGTGTGTATACAGATGATTTATGACATGTTTGTCTGAAGATTG	1620
Db				1623	AAAGTCCAGTTTGAAGGGTGTGTATACAGATGATTTATGACATGTTTGTCTGAAGATTG	1682
QY				1621	AAATCCGTTCTCTATTTTGGCTGGTACTTTGTCTGCAAAAAGGAGAAATTTGCAAGGAA	1680

RESULT 2

US-09-855-828-2
 ; Sequence 2, Application US/09855828
 ; Publication No. US20040137433A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cretech, Christopher D.
 ; APPLICANT: Jegla, Timothy J.
 ; APPLICANT: ICAGEN, Inc.
 ; TITLE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
 ; FILE REFERENCE: 018512-006010US
 ; CURRENT APPLICATION NUMBER: US/09/855,828
 ; CURRENT FILING DATE: 2001-05-14
 ; PRIOR APPLICATION NUMBER: US 60/204,445
 ; PRIOR FILING DATE: 2000-05-15
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 2703
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: complete human CNG3B nucleotide sequence
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (63)..(2492)
 ; OTHER INFORMATION: CNG3B

Query Match 100.0%; Score 2430; DB 3; Length 2703;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGTTTAAATCGCTGCAAAAGTCAACAGGTGAAGCTTATAGGAGAGAACATGAGAT	60
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QY	61	GAACAAGTCTCGTCGGATGAAGAGGCTCTCACCAAGTATCAGTCTCAGCAAAACC	120
Db	123	GAACAAGTCTCGTCGGATGAAGAGGCTCTCACCAAGTATCAGTCTCAGCAAAACC	182
QY	121	ACAGCACAGGAAGAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC	180
Db	183	ACAGCACAGGAAGAAACAAAGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC	242
QY	181	ACGTCCTGAAGAGCCACACCAACATACAGAACTCTCCAAAGAAATTTCTCTGGA	240
Db	243	ACGTCCTGAAGAGCCACACCAACATACAGAACTCTCCAAAGAAATTTCTCTGGA	302
QY	241	GATCTGACCAACCTGACCTTCAAAATGACAGCAACCACTGGAACAGTGCCAGAG	300
Db	303	GATCTGACCAACCTGACCTTCAAAATGACAGCAACCACTGGAACAGTGCCAGAG	362
QY	301	CAGAGGAATGGAACCCGGGAAGAGGTCCAAACAGCCCAACAAACCAACCCGCTGCA	360
Db	363	CAGAGGAATGGAACCCGGGAAGAGGTCCAAACAGCCCAACAAACCAACCCGCTGCA	422
QY	361	GCTCTCTTATAATGATGCGATGCCAGTACCAACCTGGTGAAGAAATTCGCT	420
Db	423	GCTCTCTTATAATGATGCGATGCCAGTACCAACCTGGTGAAGAAATTCGCT	482
QY	421	CAAGACAGCCCTCTACAGAAAGTGGTAGAGGGAGTCTCTCTCACCCGAGCC	480
Db	483	CAAGACAGCCCTCTACAGAAAGTGGTAGAGGGAGTCTCTCTCACCCGAGCC	542
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Db	543	AGCCCAACAACTGCAAGAGCCACGGCTGTACCAAGTAAAGAAAGCGATGATAGCCCA	602

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QY 1681 ATGTATATCATCAAGCATGAGAAATCCAAAGTTCTTTGGAGGCGCTCATGTACTAAAGTT 1740
Db 1743 ATGTATATCATCAAGCATGAGAAATCCAAAGTTCTTTGGAGGCGCTCATGTACTAAAGTT 1802
QY 1741 CTGGTTACTCTGAAGACTGGGTGGTGGTTTGGAGAAATCAGCCTTTAGCAGCAGGAGGA 1800
Db 1803 CTGGTTACTCTGAAGACTGGGTGGTGGTTTGGAGAAATCAGCCTTTAGCAGCAGGAGGA 1862
QY 1801 GGAAACCGTCGAATCGCAATGTGGTGGGCCACGGGTTTGGCAATCTTTAACTCTAGAC 1860
Db 1863 GGAAACCGTCGAATCGCAATGTGGTGGGCCACGGGTTTGGCAATCTTTAACTCTAGAC 1922
QY 1861 AAAAGACCCCTCCAGAAATTTCTAGTGCATTATCCAGATTCTTGAAGGATCTCTATGAAG 1920
Db 1923 AAAAGACCCCTCCAGAAATTTCTAGTGCATTATCCAGATTCTTGAAGGATCTCTATGAAG 1982
QY 1921 AAAGCCAGAGTGTCTTTAAAGCAGAAAGGCTTAAGACCCGAGAAACCCCTCCAGAAAT 1980
Db 1983 AAAGCCAGAGTGTCTTTAAAGCAGAAAGGCTTAAGACCCGAGAAACCCCTCCAGAAAT 2042
QY 1981 GATCTTGGCCCTCTCTTCCACCGAAAGAGAGACACCCAACTGTTTAAACTCTCCTA 2040
Db 2043 GATCTTGGCCCTCTCTTCCACCGAAAGAGAGACACCCAACTGTTTAAACTCTCCTA 2102
QY 2041 GGAGGCACAGGAAAGCAAGTCTTGAAGACTACTCAAAATTTGAAGGAGAGCAAGCAGCT 2100
Db 2103 GGAGGCACAGGAAAGCAAGTCTTGAAGACTACTCAAAATTTGAAGGAGAGCAAGCAGCT 2162
QY 2101 CAGAGAAAGAAATTTCTGAAGGAGAGAGGAGAAAGGAAAGAAATGAAGATAA 2160
Db 2163 CAGAGAAAGAAATTTCTGAAGGAGAGAGGAGAAAGGAAAGAAATGAAGATAA 2222
QY 2161 AAAGAAATGAAGATAAACAAAGAAATGAAGATAAAGGAAAGAAATGAAGATAA 2220
Db 2223 AAAGAAATGAAGATAAACAAAGAAATGAAGATAAAGGAAAGAAATGAAGATAA 2282
QY 2221 GATAAGGAGAGAGCAGAGAGAGCCACTGGACAGACCTGAATGTACAGCAAGTCT 2280
Db 2283 GATAAGGAGAGAGCAGAGAGAGCCACTGGACAGACCTGAATGTACAGCAAGTCT 2342
QY 2281 ATTGCAGTGGAGAGAAACCCCACTCAGTTAGAGGACAGTTTACCAGAGGACTTCT 2340
Db 2343 ATTGCAGTGGAGAGAAACCCCACTCAGTTAGAGGACAGTTTACCAGAGGACTTCT 2402
QY 2341 CGTCAATCACTCATTTATCAGATGGCTCTCTGCTGAGGGCGGAGAGGTTCTTACT 2400
Db 2403 CGTCAATCACTCATTTATCAGATGGCTCTCTGCTGAGGGCGGAGAGGTTCTTACT 2462
QY 2401 ATTGAAGTCAAGAAAGGCTAAGCAATAA 2430
Db 2463 ATTGAAGTCAAGAAAGGCTAAGCAATAA 2492

RESULT 3
US-09-855-828-16
; Sequence 16, Application US/09855828
; Publication No. US2004013743A1
; GENERAL INFORMATION:
; APPLICANT: Creech, Christopher D.
; APPLICANT: Jegia, Timothy J.
; APPLICANT: ICAGEN, Inc.
; FILE OF INVENTION: CNG3B: A Novel Cyclic Nucleotide-Gated Cation Channel
; CURRENT FILING DATE: 2001-05-14
; CURRENT APPLICATION NUMBER: US/09/855,828
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: US 60/204,445
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16

; LENGTH: 2757
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: complete CNG3B sequence derived from assembly of
; OTHER INFORMATION: PCR fragments
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (112)..(2541)
; OTHER INFORMATION: CNG3B
US-09-855-828-16

Query Match 100.0%; Score 2430; DB 3; Length 2757;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2430; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGTTTAAATCGCTGACAAAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAAATCAGAA 60
Db 112 ATGTTTAAATCGCTGACAAAAGTCAACAAGGTGAAGCCTATAGGAGAGAACAAATCAGAA 171
QY 61 GAAACAAGTCTCGTCGGAATGAAGAAGCCTCTCACCCAAAGTAATCAGTCTCAGCAAAACC 120
Db 172 GAAACAAGTCTCGTCGGAATGAAGAAGCCTCTCACCCAAAGTAATCAGTCTCAGCAAAACC 231
QY 121 ACAGCACAGGAGAGAAAAAACAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCTCAATC 180
Db 232 ACAGCACAGGAGAGAAAAAACAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAATCTCAATC 291
QY 181 AGCTCTGAAGGCCACACCAACATACAAGACAACATCTCCNAGAAAAATTTCTCTCGA 240
Db 292 AGCTCTGAAGGCCACACCAACATACAAGACAACATCTCCNAGAAAAATTTCTCTCTCGA 351
QY 241 GATCTGACACAAACCCCTGACCCCTCAAAATGCGAGAGAACCAACTGGAAACAGTGGCCAGAG 300
Db 352 GATCTGACACAAACCCCTGACCCCTCAAAATGCGAGAGAACCAACTGGAAACAGTGGCCAGAG 411
QY 301 CAGAAAGAAATGGACCCCGGGAAAGAGGTCCAAACAGCCCAACAAACAAACCCGCTGCA 360
Db 412 CAGAAAGAAATGGACCCCGGGAAAGAGGTCCAAACAGCCCAACAAACAAACCCGCTGCA 471
QY 361 GCTCCTGTTTATATAGTATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 420
Db 472 GCTCCTGTTTATATAGTATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGATGCGGAT 531
QY 421 CAAAGAAACAGCCCTCTCAAGAGAAAAAGTTGGTAGAGGAGATCTCTCTCAACCCGAAAGCC 480
Db 532 CAAAGAAACAGCCCTCTCAAGAGAAAAAGTTGGTAGAGGAGATCTCTCTCAACCCGAAAGCC 591
QY 481 AGCCCAACAACTGCAAAAGCCCAACGGCTGTACCAACAGTAAAGAAAGCGATGATAGGCA 540
Db 592 AGCCCAACAACTGCAAAAGCCCAACGGCTGTACCAACAGTAAAGAAAGCGATGATAGGCA 651
QY 541 ACAGAACATTAATCAGAGCTGTTGGTTTCAAGTCAAAAGATGCGCTTTTAAACAGATAC 600
Db 652 ACAGAACATTAATCAGAGCTGTTGGTTTCAAGTCAAAAGATGCGCTTTTAAACAGATAC 711
QY 601 TTAAGCGAAATTAAGCTTTCCAAACAGCATAGATTTCATACAGATCGACTCTATCTCCTG 660
Db 712 TTAAGCGAAATTAAGCTTTCCAAACAGCATAGATTTCATACAGATCGACTCTATCTCCTG 771
QY 661 TGGCTCTTGTGTGTCACCTCTTTGGCTTAACTGGAACTGCTGTTTATACCACTGCGCCTC 720
Db 772 TGGCTCTTGTGTGTCACCTCTTTGGCTTAACTGGAACTGCTGTTTATACCACTGCGCCTC 831
QY 721 GTCCTCCCATATCAAAACCGCAGACAACTACTACTGGCTTATTCGCGACATCATATGT 780
Db 832 GTCCTCCCATATCAAAACCGCAGACAACTACTACTGGCTTATTCGCGACATCATATGT 891
QY 781 GATATCATCTACCTTTTATGATATGCTATTATTCAGAGCCAGACCTCAGTCTTGAAGAGCA 840
Db 892 GATATCATCTACCTTTTATGATATGCTATTATTCAGAGCCAGACCTCAGTCTTGAAGAGCA 951
QY 841 GGAGACATAATAGTGGATTCAAATGAGCTAAGGAAACACTACAGGACTTCTTACAAAAATTT 900

Db 952 GGAGACATAAATAGTGGATTCAAATGAGCTAAGGAAACATACAGGACTTCTCAAAATTT 1011
Qy 901 CAGTTGGATGTCGCATCAATAATACCAATTTGATATTGCTACTCTCTCTTTGGGTTAAT 960
Db 1012 CAGTTGGATGTCGCATCAATAATACCAATTTGATATTGCTACTCTCTCTTTGGGTTAAT 1071
Qy 961 CCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTAATCATCAC 1020
Db 1072 CCAATGTTTAGAGCAAAATAGGATGTTAAAGTACACTTCAATTTTGAATTAATCATCAC 1131
Qy 1021 CTAGAGTCTAATGACAAAGCATATATCTACAGAGTTATTGCAACAACCTGGATACCTG 1080
Db 1132 CTAGAGTCTAATGACAAAGCATATATCTACAGAGTTATTGCAACAACCTGGATACCTG 1191
Qy 1081 CTGTTTATTCTGCACATAATGCTGTGTTTATTACTTGGGCTTCAAACTATGAAGAAAT 1140
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Qy 1141 GGCACCTACTAGATGGGTGATGATGGGAAAGGAAACGAGTATCTGAGATGTTATTATTGG 1200
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Qy 1201 GCAGTTCGAACCTTAATACCAATTTGCTGGCTTCCAGAACCAAACTTTATTGAAAT 1260
Db 1312 GCAGTTCGAACCTTAATACCAATTTGCTGGCTTCCAGAACCAAACTTTATTGAAAT 1371
Qy 1261 GTTTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGTCAG 1320
Db 1372 GTTTTTCAACTCTTGAATTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAATTTGTCAG 1431
Qy 1321 ATGAGAGATGTGATGGGAGCTACAGCCAAATCAGAACTACTTCCGCGCTCGATGGAT 1380
Db 1432 ATGAGAGATGTGATGGGAGCTACAGCCAAATCAGAACTACTTCCGCGCTCGATGGAT 1491
Qy 1381 GACACCAATGCTTACATGAACAAATTAATCTCAATTCCTAAACTTGTGCAAAAGCCAGTTCGG 1440
Db 1492 GACACCAATGCTTACATGAACAAATTAATCTCAATTCCTAAACTTGTGCAAAAGCCAGTTCGG 1551
Qy 1441 ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGATCTGATTTGCTTAAAG 1500
Db 1552 ACTTGGTATGAATATACATGGGACTCTCAAGAAATGCTAGATGATCTGATTTGCTTAAAG 1611
Qy 1501 ACCCTACCAACTAGCTCCAGTTAGCCCTCCGCAATGATGTAATTCAGCATCATCAGC 1560
Db 1612 ACCCTACCAACTAGCTCCAGTTAGCCCTCCGCAATGATGTAATTCAGCATCATCAGC 1671
Qy 1561 AAAGTCGACTTGTTCAGAGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTG 1620
Db 1672 AAAGTCGACTTGTTCAGAGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTG 1731
Qy 1621 AAATCCGTTCTTATTTGCTGGTGACTTTGTCTGCAAAAGGAGAAATTTGGCAAGGAA 1680
Db 1732 AAATCCGTTCTTATTTGCTGGTGACTTTGTCTGCAAAAGGAGAAATTTGGCAAGGAA 1791
Qy 1681 ATGTATATCATCAGCATGAGAGTCCAAAGTTCTTGGAGCCCTGATGGTACTTAAAGTT 1740
Db 1792 ATGTATATCATCAGCATGAGAGTCCAAAGTTCTTGGAGCCCTGATGGTACTTAAAGTT 1851
Qy 1741 CTGGTTACTCTGAAAGCTGGGTGGGTGTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA 1800
Db 1852 CTGGTTACTCTGAAAGCTGGGTGGGTGTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGA 1911
Qy 1801 GGAACCGTGCAGCTGCAATGCTGCGCCAGCGGTTTGCCAATCTTTTAACTCTAGAC 1860
Db 1912 GGAACCGTGCAGCTGCAATGCTGCGCCAGCGGTTTGCCAATCTTTTAACTCTAGAC 1971
Qy 1861 AAAAAGACCTTCCAAAGAAATTTCTAGTGCATTATCCAGATTTCTGAAAGGATCCTCATGAG 1920
Db 1972 AAAAAGACCTTCCAAAGAAATTTCTAGTGCATTATCCAGATTTCTGAAAGGATCCTCATGAG 2031
Qy 1921 AAAGCCAGAGTGTCTTTAAAGCAGAGGCTTAAGACCGGAGAGCAACCCCTCCAAAGAAA 1980

Db 2032 AAAGCCAGAGTGTCTTTAAAGCAGAGGCTAAGACCGCAGAGAAACCCCTCCAAAGAAA 2091
Qy 1981 GATCTTGGCCCTCTCTTCCCAACGAAAGAGAGACACCCAAACTGTGTTTAAAACTCTCCTA 2040
Db 2092 GATCTTGGCCCTCTCTTCCCAACGAAAGAGAGACACCCAAACTGTGTTTAAAACTCTCCTA 2151
Qy 2041 GGAGCCACAGGAAAGAGCAAGTCTTCCNAGACTACTCAAAATTCGAAGCGAGCAAGCAGCT 2100
Db 2152 GGAGCCACAGGAAAGAGCAAGTCTTCCNAGACTACTCAAAATTCGAAGCGAGCAAGCAGCT 2211
Qy 2101 CAGAAGAAAGAAAATTTCTGAAGGAGAGAGGAAAGGAAAGAAAATGAAGATAAACAA 2160
Db 2212 CAGAAGAAAGAAAATTTCTGAAGGAGAGAGGAAAGGAAAGAAAATGAAGATAAACAA 2271
Qy 2161 AAAGAAAATGAAGATAAACAAAGAAAATGAAGATAAACAGGAAAGAAAATGAAGATAAAC 2220
Db 2272 AAAGAAAATGAAGATAAACAAAGAAAATGAAGATAAACAGGAAAGAAAATGAAGATAAAC 2331
Qy 2221 GATTAAGGAGAGAGCCAGAGAGAGGCACTGGACAGACCTGAATGTACAGCAAGTCTCT 2280
Db 2332 GATTAAGGAGAGAGCCAGAGAGAGGCACTGGACAGACCTGAATGTACAGCAAGTCTCT 2391
Qy 2281 ATTGCACTCGAGGAAAGAACCCCACTCAGTTAGAAAGCAGACTTTTATCCAGAGGACTTCT 2340
Db 2392 ATTGCACTCGAGGAGAGAACCCCACTCAGTTAGAAAGCAGACTTTTATCCAGAGGACTTCT 2451
Qy 2341 CGTCAATCACTCATTTATCAGCATGCTCTTCTGTGAGGGCGGAGAGAGGTTCTTACT 2400
Db 2452 CGTCAATCACTCATTTATCAGCATGCTCTTCTGTGAGGGCGGAGAGAGGTTCTTACT 2511
Qy 2401 ATTGAAGTCAAGAAAAGGCTAAGCAATAA 2430
Db 2512 ATTGAAGTCAAGAAAAGGCTAAGCAATAA 2541

RESULT 4

US-11-060-756-2833
; Sequence 2833, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2833
; LENGTH: 1400
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-060-756-2833

Query Match 54.2%; Score 1316; DB 10; Length 1400;
Best Local Similarity 98.9%; Pred. No. 3,8e-274;
Matches 1341; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

Qy 1075 TACTTCTGTTTATCTGCACATTAAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAA 1134
Db 1 TACTTCTGTTTATCTGCACATTAAATGCTGTGTTTATTTACTGGGCTTCAAACTATGAA 60
Qy 1135 GGAATTTGGCACTACTAGATGGGTGTATGATGGGAAAGAAACGAGTATCTCAGATGTTAT 1194
Db 61 GGAATTTGGCACTACTAGATGGGTGTATGATGGGAAAGAAACGAGTATCTCAGATGTTAT 120
Qy 1195 TATTGGCAGTTCCAACTTTTAAATTACATTGGTGGCCTTCCAGAACCCAAACTTTTATTT 1254
Db 121 TATTGGCAGTTCCAACTTTTAAATTACATTGGTGGCCTTCCAGAACCCAAACTTTTATTT 180
Qy 1255 GAAATGTTTTTCAACTCTTGAATTTTTTTTCTGGAGTTTTTTTCTGGAGTTTTTGTGTTCTCCAGTTTAAAT 1314

; TITLE OF INVENTION: NUCLEOTIDE GATED (CNG) CHANNEL IN RECOMBINANT HOST
; TITLE OF INVENTION: CELLS AND USE THEREOF IN CELL BASED ASSAYS TO IDENTIFY
; FILE OF INVENTION: SMELL MODULATORS
; FILE REFERENCE: 078003-0291567
; CURRENT APPLICATION NUMBER: US/10/189,507
; CURRENT FILING DATE: 2003-02-12
; PRIOR APPLICATION NUMBER: 60/303,140
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/337,154
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-189-507-3

Query Match 23.8%; Score 577.4; DB 6; Length 2607;
Best Local Similarity 64.3%; Pred. No. 2.9e-114;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY 617 TTCCAAACAGCATAGATTTCATACAGATCGACTCTATCTCTGTGGCTTTGCTGTGCA 676
DB 782 TTCCCAAGAGCATGACCGCTGACCACTGATGATGCTCTATGCTGTGCTTTCGTGG 841

QY 677 CTCCTTGCCCTTAACCTGGAACTGCTGTTTATACCACTGCGCTCTCTCTCCCATATCAAA 736
DB 842 TGAATGCGCTTGAATGGAATCTGTGCTGATTTCCCGTGGCTTCCCTACCAGA 901

QY 737 CCGCAGACATACACTACTGCTTATTCGGGACATCATATGTGATATCATCTACTCTTT 796
DB 902 CCCCAGACAACTCACCACCTGGCTGCTGATGGAATTAACCTATGCGACCTCATCTACTCC 961

QY 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTGAAGAGGAGGAGACATAAGTGG 856
DB 962 TGGACATACCGTGTTCAGACAGCGCTGCAGTTTGTCAAGCGCGGGACATTAACGG 1021

QY 857 ATTCAATGAGCTAAGGAAACACTACAGGACTTCTACAAATTTTCAGTTGGATGCGCAT 916
DB 1022 ACAAAAGGACATGCGAAATACTACTTGAAGTCTCGCGCTTCAAGATGGACCTGCTCA 1081

QY 917 CAATATACCATTTGATTTTGGTACTCTTCTTTGGGTTTAAATCAATGTTTAGACAA 976
DB 1082 GCCTCTGCTGCTTGGATTTTCTCTATTTGAAAGTCCGTGTGAACCCCTCTCCGCTGC 1141

QY 977 ATAGGATGTTAAGTACACTTCAATTTTGAATTTAATCATCACCTAGAGTCTATAATGG 1036
DB 1142 CCGCTGTTTAAAGTACATGCGCTTCTCGAGTTTAAAGCGCCCTGGAAATCAATCCTCA 1201

QY 1037 ACAAGCATATATCTACAGAGTTATTCGAACAACTGGATCTTGTCTGTTTATTTCTGCACA 1096
DB 1202 GCAAGGCTACGTACAGGGTCATCAGGACACAGCCTACCTTCTCTACAGCTGCAIT 1261

QY 1097 TTAATGCTGCTTTTATTAAGTGGCTTCAAACTATGAAGAAATGGCACTACTAGATGG 1156
DB 1262 TGAATTCCTGCTTTTATTAAGTGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 1321

QY 1157 TGTATGATGGGGAAGGAAACGAGTATCTCAGATGTTTATTTATTTGGGCGAGTTCGAACTTTAA 1216
DB 1322 TTTACATGCGCTGGGAAACAGTTATTTGCTGTTTACTTCTGTTGGAAGACCTCA 1381

QY 1217 TTAACATTTGGTGGCTTCCAGAACCAAACTTTTATTTGAAATTTGTTTTCAACTCTTCA 1276
DB 1382 TCACCATGGGGGCTGCTGACCCCAAGACACTCTTTGAAATTTGTTTCCAGCTGCTGA 1441

QY 1277 ATTTTCTGAGTTTTTGTGTTTCTCCAGTTTAAATGGTCAGATGAGAGATGATG 1336
DB 1442 ATTAATTCACGGGCGCTTGTGCTTCTGATGATCGGACAGATGAGAGATGATG 1501

QY 1337 GAGCAGCTACAGCAATCAGAACTACTCTCCGCGCTGATGATGACACCATTTGCTTCA 1396
DB 1502 GGGCCGCCACCGGGGACAGACTACTACCGCAGCTGCAATGACAGCAGCGTGAAGTACA 1561

RESULT 8

US-10-159-563-147
; Sequence 147, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613.56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 147
; LENGTH: 4382
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-147

Query Match 23.8%; Score 577.4; DB 6; Length 4382;
Best Local Similarity 64.3%; Pred. No. 3.7e-114;
Matches 866; Conservative 0; Mismatches 481; Indels 0; Gaps 0;

QY 617 TTCCAAACAGCATAGATTTCATACAGATCGACTCTATCTCTGTGGCTTCTGCTTGTCA 676
DB 1983 TTCCCAAGCATTTGACCGCTGACCAACCTGATGTATCTTATGGCTGTTCTTCGTGG 2042


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QY 677 CTCTTCCCTATTAACCTGGAACCTGCTGTTTATACCACTGCGCCTCGCTTCCCATATCAAA 736
DB 2043 TGATGCGCTGGAATTGGAATCTGTTGCTGATTCCTCGCTGGGCTTCCCTACACGA 2102
QY 737 CCGCAGACAACATACACTACTGCTTATTTGGCGACATCATATGTGATATCATCTACTCTTT 796
DB 2103 CCGCGACACAATCCACCACTGCTGCTGATGATTTACCTATGCGACCTCATCTACTCTCC 2162
QY 797 ATGATATGCTATTTATCCAGCCAGACTCCAGTTTGTAAAGAGGAGGAGACATAATAGTGG 856
DB 2163 TGGACATACCGTGTTCAGACACCGCTGCAGTTTGTGAGAGCGGGACATCATTTACGG 2222
QY 857 ATTCAAATGAGCTAAGAAACACTACAGGACTTCTACAAAATTTCAAGTTGGATGTGCGAT 916
DB 2223 ACAAAGAGCATGCGAAATAACTACTGAAGTCTCGCGCTTCAAGATGGACCTGCTCA 2282
QY 917 CAATAATACCAATTTGATATTTGCTACTCTTCTTTGGGTTTAATCCAATGTTTAGACAA 976
DB 2283 GCCTCTCGCCTTGGATTTTCTCTATTTGAAAGTCGGTGTGAACCCCTCTCTCGCCTGC 2342
QY 977 ATAGGATGTTAAAGTACACTTTCATTTTGAATTTAATCATCACCTAGAGTCTATAATGG 1036
DB 2343 CCGCTGTTTAAAGTACATGCGCTTCTCGAGTTTAAAGCGCCTGGATCCATCCTCA 2402
QY 1037 ACAAAGCATATATCTACAGAGTTTATTCGAAACAACTGGATCTTGTGTTTATTTCTGCACA 1096
DB 2403 GCAAAGCTACGTGTACAGGTCATCAGGACACAGCTACCTTCTCTACAGCCTGCAT 2462
QY 1097 TTAATGCTGTGTTTATTTACTGGCTTCAAACTATGAAGAAATTTGGCACTACTAGATGG 1156
DB 2463 TGAATTTCTGTCTTTATTTACTGGGCATCGGCCCTATCAGGCGCTCGGCTCCACTCTGGG 2522
QY 1157 TGATGATGGGAAGAAACGAGTATCTGAGATGTTTATTTATGCGCAGTTTGAACCTTTAA 1216
DB 2523 TTTAGATGCGGTGGGAAACAGTTATATTCGCTGTTACTTGTGTGTAAGACCTCA 2582
QY 1217 TTACCAATTTGCTGCGCTTCCAGAACCAAACTTTATTTGAAATTTGTTTTCAACTCTGA 1276
DB 2583 TCACCATCGGGGGCTGCTTGCATGCCCAAGACACTCTTTGAAATTTGCTTCCAGCTGCTGA 2642
QY 1277 ATTTTCTTCTGAGTTTTTGTGTTTCTCCAGTTTAAATGTTGTCAGATGAGAGATGTGATTG 1336
DB 2643 ATTTATTTACGCGGCTGTTTGTCTCTGTGATGATCGGACAGATGAGAGATGTGGTAG 2702
QY 1337 GAGCAGCTACAGCAATTCAGAACTACTTTCGCGCTGCTGATGGATGACACCATTTGCCTACA 1396
DB 2703 GGCGCGCACCGGGGACACCTTACTACCGAGCTGCTGACGACGACGCTGAGTACA 2762
QY 1397 TGAACAATTAATCTCAATTCCTAAACTTTGTGCAAAAGCGAGTTTCGAGCTTGGTATGAATATA 1456
DB 2763 TGAATTTCTAAGATCCCAAGTCCGTCAGAACCGCTCAAGACCTGGTACGAGTACA 2822
QY 1457 CATGGGACTCAAGAAATGCTAGATGAGTCTGATTTGCTTAAAGACCTTACCAACTACGG 1516
DB 2823 CCTGGCACTCGCAGGATGCTGATGAGTCAGAGCTGATGGTGCAGCTTTCAGACAAGA 2882
QY 1517 TCCAGTTTAGCCCTCGCCATTTGATGTGAATTTTCAGCATCATCAGCAAAAGTCGACTTTTCA 1576
DB 2883 TCGGCTGGAACCTCGCCATCGACGTGAATCTACAACTATCGTTAGCAAAAGTCGACTTTTC 2942
QY 1577 AGGTTGTGTATACACAGATGATTTATGACATGTTTGTGTAAGATTTGAAATTCGCTTCTTATT 1636
DB 2943 AGGCTGTGACCGGCAGATGATCTTTGACATGCTGGAAGAGCTTCGCTCTGTTGTCTACC 3002
QY 1637 TGCCTGTGTACTTTGTCTGMAAAGGAGAAATTTGCAAGGAAATGATATATCATCAAGC 1696
DB 3003 TGCCCAACGACTATGTGTGCAAGAGGGGAGATCGGCCGTGGAGATGTACATCATCCAGG 3062
QY 1697 ATGAGAAAGTCCAAGTTCTTGGAGGCCCTGATGTGTAAGTTCTGTTACTCTGAAAG 1756
DB 3063 CAGGCAAGTGCAGGTTCTTTGGGCGGCCCTGATGGAATAATCTGTGCTGGTACGCTGAAG 3122
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QY 1757 CTGGGTCGGTCTTTGGAGAAATCAGCCTTCTAGCAGCAGGAGGAAACCGTCGAACCTG 1816
DB 3123 CTGGATCTGTGTTTGGAGAAATAAGCTTCTGCTGCTGTTGGGGCGGGAAACCGCGCACCG 3182
QY 1817 CCAATGTGTGTCGCCACACGGGTTTGGCAATCTTTTAACTCTTAGACAAAAAGACCTTCCAAG 1876
DB 3183 CCAACGTGTGTGCGCACGGGTTTACCACTCTTCTCATCTGATTAAGAAGGACCTTCAATG 3242
QY 1877 AAATTTAGTGCATTTATCCAGATTTCTGAAGGATCTCTATGAAGAAAGCCAGAGTCTTT 1936
DB 3243 AGATTTTGGTGCATTTATCTGAGTCTCAGAAGTTTACTCCGGAAGAAAGCCAGGCGCATGC 3302
QY 1937 TAAACAGAGGCTTAAGACCGCAGAG 1963
DB 3303 TGAGAAGCAACAATAAGCCCAAGGAGG 3329

RESULT 9
US-10-450-763-27462
; Sequence 27462, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 27462
; LENGTH: 3811
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (2009)..(3808)
; OTHER INFORMATION: 99% homologous to Homo sapiens cyclic nucleotide-gated cation
; OTHER INFORMATION: channel, accession number L15296, Smith-Waterman Score=3168.
US-10-450-763-27462

Query Match 23.6%; Score 573.6; DB 9; Length 3811;
Best Local Similarity 64.6%; Pred. No. 2.3e-113;
Matches 855; Conservative 0; Mismatches 469; Indels 0; Gaps 0;

QY 640 ACAGATCGACTCTATCTCTGTGGCTTCTTGTGTCACCTTTCGCTTATACTGGAACCTGC 699
DB 2009 ACAGACTGATGTATGCTCTATGCTTCTTCTGCTGATGCTTGGAAATTTGGAACCTGT 2068
QY 700 TGGTTTATACCACTGCGCTCGTCTTCCCATATCAAAACCGCAGACACATACACTACTGG 759
DB 2069 TGGCTGATTTCCGCTGGGCTTCCCTTACGACCCCGGACAAACATCCCACTCTG 2128
QY 760 CTATTTCGCGACATCATATGTGATATCATCTACTTTTATGATATGCTATTATTCAGCCCC 819
DB 2129 CTGCTGATGATTTACCTATGCGACCTCATCTACTTCTCTGGACATCACCCTGTTCCAGACA 2188
QY 820 AGACTCCAGTTTGTAAAGAGGAGGAGACATAAATAGTGGATTCAAATGAGCTTAAGGAAACAC 879
DB 2189 CGCTCGAGTTTGTGAGGCGGGGACATCATTCGACAAAAAAGGACATCGCAATAAAC 2248
QY 880 TACAGACTTCTACAAAAATTTAGTTGGATGTCGCACTCAATAATACCATTTGATATTTC 939
DB 2249 TACCTGAAGTCTCGCGCTTCAAGATGGACCTCTCAGCCCTCGCTTGGATTTTCTC 2308
QY 940 TACCTCTCTTCTGGTTTAAATCCAATGTTTATAGACAAATAGGATGTTTAAAGTACACTTCA 999
DB 2309 TATTTGAAGTCGGTGTGAACCCCTCTCTCGGCTGCTGTTTAAAGTACATGCCC 2368
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QY 1000 TTTTGTGAATTTAATCATCACCTAGAGTCTATAATGGAACAAGCATATATCTACAGAGTT 1059
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2369 TTCTTCGAGTTTAAACAGCGCCTGGAAATCCATCCTCAGCAAGCCCTACGTGTACAGGGTC 2428
QY 1060 ATTCGACAACTGGATACCTTGCTGTTTATTCGACATTAATGCTGCTGTTTATTACTGG 1119
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2429 ATCAGACACACAGCCCTACCTTCTACAGCCCTGCATTTGAATTCCTGCTTATTACTGG 2488
QY 1120 GCTTCAAACTAAGAGGAATTCGCACCTACTAGATGGGTGTATGATGGGGAAGGAACGAG 1179
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2489 GCATGGCCTATCAGGCGCTCGCTCCACTCACTGGGTTTACATGGCGTGGGAACAGT 2548
QY 1180 TATCTGAGATGTTATTTATTTGGGAGTTTGAACCTTTTAAATACCATTGGTGGCCTTCCAGAA 1239
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2549 TATATTCGCTGTACTACTTGTGTGAAGACCCCTCATCACCATCGGGGGCTGCCTGAC 2608
QY 1240 CCACAACTTTATTTGAATTTGTTTCAACTCTTGAATTTTTCCTGGAGTTTGTG 1299
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2609 CCAAGACACTCTTTGAATTTGCTTCCAGCTGCTGAATTTATTCAGGGCGTCTTTGCT 2668
QY 1300 TTCTCCAGTTTAAATGGTCAGATGAGAGATGTGATTGGAGCAGCTACAGCCAAATCAGAAC 1359
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2669 TTCTCTGTGATGATCGGACAGATGAGAGATGTGATTAGGGGCCGCCACCGGGGACAGACC 2728
QY 1360 TACTTCCGCGCTGCATGATGACACCATTTGCTTACATGAACAAATTTACTTCCATAA 1419
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2729 TACTACCGCAGCTGCATGACAGCAGCGGTGAAGTACATGAATTTCTACAAAGATCCCAAG 2788
QY 1420 CTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATACATGGGACTCTCAAGAATGCTA 1479
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2789 TCGGTGCAGAACCGGCTCAAGACCTGGTACGAGTACACCTGGCAGCTCGCAAGCATGCTG 2848
QY 1480 GATGAGTCTGATTTGCTTAAAGACCCCTACCAACTACCGGTTCAGTTAGCCCTCGCATTTAT 1539
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2849 GATGAGTCAGAGCTGATGTGTGAGCTTCCAGACAAGATCGGCTGAGCTCGCATTCGAC 2908
QY 1540 GTGAATCTCAGCATCATCAGCAAGTCGACTTGTTCAGGGTTGTGATACACAGATGATT 1599
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2909 GTGAATCAACAATCGTTAGCAAGTCGCACCTTTTCAGGGCTGTGACCGGCAGATGATC 2968
QY 1600 TATGACATGTTGCTAAGATTGAAATCCGTTCTCTATTGCTGGTGACTTTGCTGCAAA 1659
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
2969 ATTGACATGCTGAAGAGGCTTCGCTCTGTGTCTACCTGCCCAAGCACTATGTGTCAAG 3028
QY 1660 AAGGAGAAATTTGGCAAGGAATGTATATCATCAAGCATGGAGAGTCCAAAGTTCTTGA 1719
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3029 AAGGGGAGATCGGCCGTGAGATGTACATCATCCAGGCAAGGCAAGTGCAGGCTTTGGGC 3088
QY 1720 GGCCTGTGTTGTTAAAGTTCTGTTTACTTGAAGCTGGGTCGGTGTTCGAGAAATC 1779
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3089 GGCCTGTGTTGGAATAATCTGTGCTGTGAGCGCTGAAAGCTGGATCTGTGTTTGGAGAAAT 3148
QY 1780 AGCCTTCTAGCAGCAGGAGGGAACCGTGCNACTGCCAATGTGTGTGCGCCACCGGTTT 1839
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3149 AGCTTGTGCTGTTTGGGGGGGGAAACCGCGCAACCGCAACGTGTGTGCGCACCGGTTT 3208
QY 1840 GCAATCTTTTAACTCTAGACAAAAGACCCCTCCAAAGAAATTTCTAGTGCATTATCCAGAT 1899
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3209 ACCAACCCTTTCATCTCTGATAGAAGGACCTGATAGATTTTGTGCTATCTCTGAG 3268
QY 1900 TCTGAAAGATCCTCATGAAGAAAGCCAGAGTGTCTTTTAAAGCAGAGGCTTAAGACCGCA 1959
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
3269 TCTCAGAGTTACTTCGGAAGAAAGCCAGGCGCATGCTGAGAAGCAACAATAAGGCCAAG 3328
QY 1960 GAAG 1963
Db ||| |||
3329 GAGG 3332
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RESULT 10
US-10-450-763-11960
; Sequence 11960, Application US/10450763

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; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 11960
; LENGTH: 2244
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (130)..(648)
; OTHER INFORMATION: 99% homologous to Homo sapiens cone photoreceptor cyclic
; OTHER INFORMATION: nucleotide-gated channel beta subunit, accession number
; OTHER INFORMATION: AF272900.Smith-Waterman Score=917.
US-10-450-763-11960
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Query Match 21.3%; Score 518; DB 9; Length 2244;
Best Local Similarity 94.7%; Pred. No. 1.9e-101;
Matches 536; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 287 GAACAGTCCAGAGCAGAGGAAGAAATGGACCCCGGAAAGAGGTCCAAACAGCCCAAAA 141
Db 83 GCAAACTATCATCAAGCAGAGAAACCAACACCGCATGTTCTCACACACAGCCCAAAA 142
QY 347 ACAACCCGCTGCAGCTCTGTTTATAATGATGATGCGATGCCAGTGCAGCTACACAACCTGG 406
Db 143 ACAACCCGCTGCAGCTCTGTTTATAATGATGATGCGATGCCAGTGCAGCTACACAACCTGG 202
QY 407 TGAAGAAGTGGTCAAGAGAACAGCCCTCTCAAGAAAAAGTTGTTAGAGGAGATCTCT 466
Db 203 TGAAGAAGTGGTCAAGAGAACAGCCCTCTCAAGAAAAAGTTGTTAGAGGAGATCTCT 262
QY 467 CTTACCCGAGCCAGCCCAACAACTGCAAGCCCAACCGCTGTACCAAGTAAAGAAA 526
Db 263 CTTACCCGAGCCAGCCCAACAACTGCAAGCCCAACCGCTGTACCAAGTAAAGAAA 322
QY 527 GCGATGATAAGCCACAGAACATTTACTACAGGCTGTTGTTGTTCAAGTCAAAAAGATGC 586
Db 323 GCGATGATAAGCCACAGAACATTTACTACAGGCTGTTGTTGTTCAAGTCAAAAAGATGC 382
QY 587 CTTTAAACAGAGTACTTAAAGCGAATTTAAACTTCCAAACAGATAGATTATACACAGATC 646
Db 383 CTTTAAACAGAGTACTTAAAGCGAATTTAAACTTCCAAACAGATAGATTATACACAGATC 442
QY 647 GACTCTATCTCTGTGGCTCTTGTGTTGTCACCTTTTGCCTATAACTGGAACCTGCTGTTTA 706
Db 443 GACTCTATCTCTGTGGCTCTTGTGTTGTCACCTTTTGCCTATAACTGGAACCTGCTGTTTA 502
QY 707 TACCACTGGGCTGCTCTTCCCATATCAAAACCGAGACAAACATACACTACTGGCTTATTG 766
Db 503 TACCACTGGGCTGCTCTTCCCATATCAAAACCGAGCAACATACACTACTGGCTTATTG 462
QY 767 CGGACATCATATGTCATATCATCTTACCTTTATGATATCTATTATTCAGCTTCTT 846
Db 563 CGGACATCATATGTCATATCATCTTACCTTTATGATATCTATTATTCAGCTTCTT 622
QY 827 AGTTTGTAAAGGAGGAGACATAATA 852
Db 623 AGTTTGTAAAGGAGGAGACATAATA 648
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RESULT 11

Db	1622	CTCAGTTTGTGGTATTGACGATGGCAGCACCTTCGGTGAGATCAGCATTTCTTAACATTA	1681
Qy	1787	TAGCAGCAGGAGGAGGAAACCGTCGAACTGCCAATGTGGTGCCACCGGTTTGCCCAATC	1846
Db	1682	AAGGGAGCAAAAGCTGGCAATCGAAGNACGGCCCAATATTAAAGTATTGGCTACTCAGACC	1741
Qy	1847	TTTTAACTCTAGACAAAAAGACCTTCCAAAGAAATTCAGTGCAATTATCCAGATTCTGAAA	1906
Db	1742	TGTTCTGTCTCTCAAAAGATGACCTCATGGAAGCTCTAACTGAGTACCCAGATGCCAAAA	1801
Qy	1907	GGATCCTCATGAAGAAGCCAGAGTGCTTTTAAAGCAGAGGCT	1950
Db	1802	CTATGCTAGAGAAAAAGGGAAGCAAAATTTTAATGAAGATGGT	1845

Search completed: December 23, 2005, 23:51:25
Job time : 1738 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 17:34:16 ; Search time 312 Seconds
(without alignments)
4041.860 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 4168288 seqs, 259477437 residues

Total number of hits satisfying chosen parameters: 8336576

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.New.*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	162.2	6.7	841	6	US-10-750-185-26200
2	126.2	5.2	1603	6	US-10-750-185-26195
C 3	80.4	3.3	1687	6	US-10-750-185-47568
C 4	72.2	3.0	380749	6	US-10-995-561-13216
C 5	71.6	2.9	600	6	US-10-750-185-20334
C 6	71.6	2.9	1442	6	US-10-750-185-26196
C 7	67	2.8	118996	6	US-11-121-086-84
C 8	65.2	2.7	184868	7	US-11-121-086-88
C 9	64.4	2.7	191350	6	US-10-857-780-4
C 10	64	2.6	201	6	US-10-995-561-21234
C 11	63.4	2.6	173602	7	US-11-121-086-25
C 12	62.8	2.6	201	6	US-10-995-561-21194
C 13	62.8	2.6	201	6	US-10-995-561-21195
C 14	62.8	2.6	201	6	US-10-995-561-21351
C 15	62.8	2.6	28037	6	US-10-995-561-13220
C 16	61.8	2.5	65723	6	US-10-995-561-13200
C 17	61.6	2.5	901	6	US-10-750-185-47572
C 18	61.6	2.5	150468	7	US-11-112-908-56
C 19	61.6	2.5	193789	7	US-11-112-908-55
C 20	61.4	2.5	2138	6	US-10-750-185-60698
C 21	61.2	2.5	201	6	US-10-995-561-21291
C 22	61.2	2.5	207908	7	US-11-112-908-21
C 23	61.2	2.5	212805	7	US-11-112-908-19

ALIGNMENTS

RESULT 1

US-10-750-185-26200
; Sequence 26200, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26200
; LENGTH: 841
; TYPE: DNA
; ORGANISM: Bovine 19866881614227
US-10-750-185-26200

Query Match 6.7%; Score 162.2; DB 6; Length 841;
Best Local Similarity 77.3%; Pred. No. 1.9e-25;
Matches 197; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
QY 2176 AAACAAAAGAAAATGAAGATAAGGAAAAGAAAATGAAGATAAGGATAAGGATAAGGAGAG 2235
DB 395 AAAGACCAAAACCAGGAGAGGAGGATAAGGAAAAGAAATCTGAAGATAAGGAGAGCA 454
QY 2236 CCAGAGAGAGGACCTGGACAGACCTGAATGTACAGCAAGTCTCTATTGCGAGTGAGGAA 2295
DB 455 ACAGCAGAGAAACCACTTGAACATCCAAATGTGAAACGAGTTCATTTACAGCGGAGGAA 514
QY 2296 GAACCCCACTCAGTTAGAGGACAGTTTTTACCAGAGGGAGTCTCTCTCAATCACTCATTT 2355
DB 515 GCGCCCCAGGCAACTAGAAAGGCGGTTTTTCCCGAGAGGAACATCCCGTCACTCCCTCATC 574
QY 2356 ATCAGCATGCTCTCTCTGCTGAGGCGGAGAGAGGTTCTTACTATTGAGTCAAGAA 2415
DB 575 ATCAGCATGCTCTCTCTGCGAGGCGGAGAGGTTCTGACGATCGAAGTCAAGAA 634


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QY 2416 AAGGCTAAGCAATAA 2430
; TYPE: DNA
; ORGANISM: Bovine 19866881478981
; LENGTH: 1687
; US-10-750-185-47568

Db 635 AAGGCTAAGCAATAA 649

RESULT 2
US-10-750-185-26195
; Sequence 26195, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 26195
; LENGTH: 1603
; TYPE: DNA
; ORGANISM: Bovine 19866880906828
US-10-750-185-26195

Query Match 5.2%; Score 126.2; DB 6; Length 1603;
Best Local Similarity 77.9%; Pred. No. 1.1e-17;
Matches 152; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 1291 GTTTTGTGTTCTCCAGTTTAATTCGTGATGAGAGATGATTCGAGCAGCTACAGCC 1350
Db 732 GGTGTGGAGTGATCATATATTTTGGTTTTAGATGCAAGAGCTAAATTTGGGCGGCTACAGCC 791

QY 1351 AATCAGAACTACTTCGGCGCTTCGATGATGACACCATTCCTACATGAACAATTAATCTCC 1410
Db 792 AATCAGAACACTTCGCGATCTGCGATGATGATGATGATGATGATGATGATGATGATGATGAT 851

QY 1411 ATTCTAACTTGTGCAAAAGCGAGTTCCGACTTGGTATGAATATACATGGGACTCTCAA 1470
Db 852 ATTCCTAAGACTGTGCAGAAATCCGGTCCGGACTTGGTATGAATATACATGGGCGCTCTCAA 911

QY 1471 AGAATGCTAGATGAG 1485
Db 912 GGAATGCTAGGTAAG 926

RESULT 3
US-10-750-185-47568/c
; Sequence 47568, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 47568
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; LENGTH: 1687
; TYPE: DNA
; ORGANISM: Bovine 19866881478981
; US-10-750-185-47568

Query Match 3.3%; Score 80.4; DB 6; Length 1687;
Best Local Similarity 67.1%; Pred. No. 5.9e-08;
Matches 114; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 1318 CAGATGAGAGATGTGATTGGAGCAGCTACAGCAATCAGAACTACTTCGCGCCTGCATG 1377
Db 1626 CAGATGAGAGAGCTAGTGGGGCCGCCACCGGGGACAGACCTACTACCGCAGCTGCATG 1567

QY 1378 GATGACACCATTTGCCCTACATGAACAAATTAATCTCCATTCCTAAACTTGTGCAAAAGCGAGTT 1437
Db 1566 GACAGCACCGTGAAGTATATGAACCTTCTACAAGATCCCCAGGTCCGTGCAGAACCGGCTC 1507

QY 1438 CGGACTTGGTATGAATATACATGGGACTCTCTCAAGAATGCTAGATGAGTC 1487
Db 1506 AAGACCTGGTACGAATACACCTGGCACTCCCAAGGCGATGCTGGGTAAGAC 1457

RESULT 4
US-10-995-561-13216/c
; Sequence 13216, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; FILE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13216
; LENGTH: 380749
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(380749)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1
US-10-995-561-13216

Query Match 3.0%; Score 72.2; DB 6; Length 380749;
Best Local Similarity 56.2%; Pred. No. 2.5e-05;
Matches 131; Conservative 2; Mismatches 100; Indels 0; Gaps 0;

QY 2088 AGAGCAAGCAGCTCAGAAAGAAAGAAATTTCTGAAGGAGCAGAGGAAAGGAAAGAAAGAAA 2147
Db 65936 AGAGCAAGACTCTGTCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAA 65877

QY 2148 TGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAGAAATGAAGATAAAGGAAAGAA 2207
Db 65876 AGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAA 65817

QY 2208 AAATGAAGATAAAGATAAAGGAGAGCCAGAGAGCCAGAGAGCCACTGGACAGACCTGAATG 2267
Db 65816 GAAGGAARGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGAAA 65757

QY 2268 TACAGCAAGTCCTATTTCAGTGGAGGAAGAACCCCACTCAGTTAGAGGACAG 2320
Db 65756 GAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 65704

RESULT 5
US-10-750-185-20334/c
; Sequence 20334, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
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; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21351
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-21351

Query Match      2.6%; Score 62.8; DB 6; Length 201;
Best Local Similarity 59.6%; Pred. No. 0.00014;
Matches 106; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 2070 ACTACTCAAATTTGAACGCGAGAGCAAGCAGCTCAGAGAAAGAAAAATTTCTGAAGGAGGAGA 2129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179  ACTTTGMAAATAAAGAAAGACGAGACGACGACGAAGAAGATAAGAGGAAGAGGAAGAAGA 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2130 GGAAGAGGAAAGAAAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAGAAA 2189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119  GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2190 TGAAGATAAGCAAGAAAGAAATGAAGATAAAGCAAGAGAGCCAGAGAGAGAG 2247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59   GGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2

RESULT 15
US-10-995-561-13220/c
; Sequence 13220, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13220
; LENGTH: 28037
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13220

Query Match      2.6%; Score 62.8; DB 6; Length 28037;
Best Local Similarity 53.5%; Pred. No. 0.00092;
Matches 121; Conservative 4; Mismatches 101; Indels 0; Gaps 0;

QY 2070 ACTACTCAAATTTGAACGCGAGAGCAAGCAGCTCAGAGAAAGAAAAATTTCTGAAGGAGGAGA 2129
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Db 9276 ACTTTGMAAATAAAGAAAGACGAGACGACGCGYAGAAGATAAGAGGAAGAGGAAGAAGA 9217
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QY 2130 GGAAGAGGAAAGAAAAATGAAGATAAACAAGAAAGAAATGAAGATAAACAAGAAAGAAA 2189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9216 GGAAGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9157
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2190 TGAAGATAAGCAAGAAAGAAATGAAGATAAAGCAAGAGAGCCAGAGAGAGAGAGAGAGCC 2249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 9156 RGARGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 9097
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 2250 ACTGCACAGACCTGAATGTACAGCAAGTCCTATTTCAGTGGAGGAA 2295
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Db 9096 GGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 9051
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Job time : 316 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 23, 2005, 16:49:01 ; Search time 11791 Seconds
(without alignments)
11714.932 Million cell updates/sec

Title: US-09-855-828-3
Perfect score: 2430
Sequence: 1 agtcttaaatcgtgacaaa.....aagaaaaggctgaagcaataa 2430

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb_env.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pr.*

9: gb_ro.*

10: gb_sts.*

11: gb_sy.*

12: gb_un.*

13: gb_vl.*

14: gb_htg.*

15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2430	100.0	4369	8 AF272900	Homo sapi
2	2049.4	84.3	2135	8 AF228520	Homo sapi
3	1682.2	69.2	2826	4 AF490511	Canis fam
4	1362.4	56.1	4710	9 MMU243572	Mus muscu
5	853.4	35.1	1350	6 CQ716885	Sequence
6	577.4	23.8	3025	8 HUMCNGCCB	Homo sapien
7	577.4	23.8	3408	8 HUMCNGCCA	Homo sapien
8	577.4	23.8	4033	8 HSU58837	Human cGMP-
9	577.4	23.8	4382	8 AF042498	Homo sapi
10	575.8	23.7	4320	6 CQ715550	Sequence
11	575.2	23.7	4763	9 BC045114	Mus muscu
12	572.2	23.5	3083	4 AF074012	Bos tauru
13	572.2	23.5	3090	4 AF074013	Bos tauru
14	572.2	23.5	3253	4 BTNCGACGN	B. taurus mR
15	572.2	23.5	3290	4 AF074014	B. taurus mR
16	572.2	23.5	4282	4 BTCPNGCL	B. taurus mR
17	569.6	23.4	4238	9 RNCNG41	Rattus no
18	568	23.4	3236	6 CQ880122	Sequence

19	568	23.4	3236	9 RNCNG43	AJ000515 Rattus no
20	568	23.4	3328	9 AF068572	AF068572 Rattus no
21	330	13.6	205816	8 AC013751	AC013751 Homo sapi
22	237.4	9.8	2511	2 CEU73476	U73476 Caenorhabdi
23	223	9.2	3275	6 CQ598668	Sequence
24	223	9.2	3358	2 BT001439	BT001439 Drosophill
25	217.8	9.0	3099	9 BC046523	BC046523 Mus muscu
26	196.2	8.1	441	9 AF015728	AF015728 Rattus no
27	187.4	7.7	1709	2 AY060725	AY060725 Drosophill
28	181.2	7.5	2061	4 SSU85404	U85404 Sus scrofa
29	181.2	7.5	2487	6 CQ716337	CQ716337 Sequence
30	181.2	7.5	2857	8 S42457	S42457 CNGC-rod ph
31	176.8	7.3	2697	4 CFACGMP	X99914 C.familiari
32	176.8	7.3	2717	4 CFU83905	U83905 Canis famli
33	176.4	7.3	2500	6 AX930698	AX930698 Sequence
34	176.4	7.3	2500	8 HUMCNGP	M84741 Human CGMP-
35	173.6	7.1	2682	4 BTGCMPCP	M84741 Human CGMP-
36	169.8	7.0	1674	8 AF547222	AF547222 Homo sapi
37	169.8	7.0	181804	8 AC107068	AC107068 Homo sapi
38	166.6	6.9	178672	14 AC161820	AC161820 Pan trogl
39	166.6	6.9	219112	14 AC164974	AC164974 Pan trogl
40	166.4	6.8	2297	9 MMU19717	U19717 Mus musculu
41	164.8	6.8	2474	9 MUSCNGC	M84742 Mus musculu
42	162.4	6.7	6312	2 AF091302	AF091302 Limulus p
43	162.2	6.7	229715	14 AC161933	AC161933 Bos tauru
44	162	6.7	274861	14 AC154999	AC154999 Bos tauru
45	161.4	6.6	58409	9 AL772281	AL772281 Mouse DNA

ALIGNMENTS

RESULT 1	AF272900	4369 bp	mRNA	linear	PRI 29-AUG-2000
LOCUS	AF272900	Homo sapiens cone photoreceptor cyclic nucleotide-gated channel			
DEFINITION	AF272900	beta subunit (CNGB3) mRNA, complete cds.			
ACCESSION	AF272900	AF272900.1	GI:9247065		
VERSION	AF272900				
KEYWORDS	AF272900				
SOURCE	AF272900	Homo sapiens (human)			
ORGANISM	AF272900	Homo sapiens			
REFERENCE	AF272900	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	AF272900	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
TITLE	AF272900	Hominidae; Homo.			
JOURNAL	AF272900	1 (bases 1 to 4369)			
PUBLISHED	AF272900	Kohl, S., Baumann, B., Broghammer, M., Jagle, H., Sieving, P.,			
REFERENCE	AF272900	Kellner, U., Spagal, R., Anastasi, M., Zrenner, E., Sharpe, L.T. and			
AUTHORS	AF272900	Wissinger, B.			
TITLE	AF272900	Mutations in the CNGB3 gene encoding the beta-subunit of the cone			
JOURNAL	AF272900	photoreceptor cGMP-gated channel are responsible for achromatopsia			
PUBLISHED	AF272900	(ACHM3) linked to chromosome 8q21			
REFERENCE	AF272900	Hum. Mol. Genet. 9 (14), 2107-2116 (2000)			
AUTHORS	AF272900	2 (bases 1 to 4369)			
JOURNAL	AF272900	Wissinger, B. and Kohl, S.			
PUBLISHED	AF272900	Direct Submission			
REFERENCE	AF272900	Submitted (30-MAY-2000) University Eye Hospital, Molecular Genetics			
AUTHORS	AF272900	Laboratory, Auf der Morgenstelle 15, Tuebingen D-72076, Germany			
TITLE	AF272900	Location/Qualifiers			
JOURNAL	AF272900	1. .4369			
PUBLISHED	AF272900	/organism="Homo sapiens"			
REFERENCE	AF272900	/mol_type="mRNA"			
AUTHORS	AF272900	/db_xref="taxon:9606"			
JOURNAL	AF272900	1. .4369			
PUBLISHED	AF272900	/gene="CNGB3"			
REFERENCE	AF272900	47. .2476			
AUTHORS	AF272900	/codon_start=1			
JOURNAL	AF272900	/gene="CNGB3"			
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REFERENCE	AF272900	channel beta subunit"			
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JOURNAL	AF272900	/db_xref="GI:9247066"			

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ORIGIN

		Query March	100.0%;	Score 2430;	DB 8;	Length 4369;
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Qy	61	GAACAAAGTTCGTGCGAATGAAGAAGGCTCTCACCCAAAGTAATCAGTCTCAGCAAAACC	120			
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Db	227	ACGTCTGGAAGGCCACACCAACATACAAAGCAAACTCTCCAAGAAAAATTCCTCTGGA	286			
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Db	287	GATCTGACCAAAACCCGTGACCCCTCAAAATGCAGAGAAACAACTGGAAACAGTGCCAGAG	346			
Qy	301	CAGAAGGAATGGAACCCCGGGAAGAGGTCCAAACAGCCCAACAAAAACAACCCGCTGCA	360			
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Qy	361	GCTCCTGTTTAAATGAGTATGCCGATGCCAGCTACACAACTGGTGAAGAAAGATGCGT	420			
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Qy	421	CAAGAAGACGCCCTCTACAAGAAAAAGTTGGTAGAGGAGATCTCTCTCAACCCGAAGCC	480			
Db	467	CAAGAAGACGCCCTCTACAAGAAAAAGTTGGTAGAGGAGATCTCTCTCAACCCGAAGCC	526			
Qy	481	AGCCCAACAACTGCAAGCCCAAGCGTGTACACCAAGTAAAGAAAGCGATGAAGCCA	540			
Db	527	AGCCCAACAACTGCAAGCCCAAGCGTGTACACCAAGTAAAGAAAGCGATGAAGCCA	586			
Qy	541	ACAGAACATTAATAAGGCTGTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGAGTAC	600			
Db	587	ACAGAACATTAATAAGGCTGTGTGGTTCAAAGTCAAAAGATGCTTTAAACAGAGTAC	646			
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Db	647	TTAAAGCGAATTAACCTTCAAAACAGCATAGATTTCATACACAGATCGACTCTATCTCTG	706			
Qy	661	TGGCTCTTGCTTGTCACCTTTCGCTTAACTGGAACCTGCTGGTTTATACCACTGCGCCTC	720			
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Qy	721	GTCTTCCCATATCAAAACCGCAGACAAATACACTACTGGCTTTATTGCGGACATCATATGT	780			
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QY	841	GGAGACATAANTAGTGGATTCAATAGCAGCTAAGGAACACTACAGGACTTCTACAAAAATTT	900
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QY	1081	CTGTTTATTTCTGCACATTAATGCCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTT	1140
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QY	1321	ATGAGAGATGTAATGGAGCAGCTACAGCCAATCAGAACTACTTCCGCGCTTCGATGATGAT	1380
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QY	1381	GACACATTTGCTACATGAACTACTCTCAATCTCTAACTTGTGCAAAAGCGAGTTTCGG	1440
Db	1427	GACACATTTGCTACATGAACTACTCTCAATCTCTAACTTGTGCAAAAGCGAGTTTCGG	1486
QY	1441	ACTTGGTATGAATATACATGGGACTCTCAAAAGATGCTAGATGAGTCTGATTGCTTAAAG	1500
Db	1487	ACTTGGTATGAATATACATGGGACTCTCAAAAGATGCTAGATGAGTCTGATTGCTTAAAG	1546
QY	1501	ACCTTACCAACTACGGTCCAGTTAGCCCTCGCCATTTGATGTGAACCTTCAGCATCATCAGC	1560
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QY	1561	AAAGTCGACTTGTTCAGAGGTTTGATACACAGATGATTTATGACATGTTGCTAAGATTG	1620
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QY	1621	AAATCCGTTCTCTATTTTGCCTGGTGACTTGTCTGCAAAAAGGGAGAAATTTGGCAAGAA	1680
Db	1667	AAATCCGTTCTCTATTTTGCCTGGTGACTTGTCTGCAAAAAGGGAGAAATTTGGCAAGAA	1726
QY	1681	ATGATATATCATCAAGCATGGAGAAAGTCCAAGTTCTTGAGGCCCTTGATGGTACTTAAAGTT	1740
Db	1727	ATGATATATCATCAAGCATGGAGAAAGTCCAAGTTCTTGAGGCCCTTGATGGTACTTAAAGTT	1786
QY	1741	CTGGTTACTCTGAAAGCTGGGTTCGGTGTTCGAGAAATTCAGCCTTCTAGCAGCAGGAGA	1800
Db	1787	CTGGTTACTCTGAAAGCTGGGTTCGGTGTTCGAGAAATTCAGCCTTCTAGCAGCAGGAGA	1846
QY	1801	GGAAACCGTCCAACTGCCAATGTGGTGGCCCAACGGGTTTGCCAAATCTTTTAACTCTAGAC	1860
Db	1847	GGAAACCGTCCAACTGCCAATGTGGTGGCCCAACGGGTTTGCCAAATCTTTTAACTCTAGAC	1906
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1921	QY		AAAGCCAGAGTGTCTTTAAAGCAGAGGCTTAAGACCGCAGACCAACCCCTCCAAGAAAA	1980
1967	DB		AAAGCCAGAGTGTCTTTAAAGCAGAGGCTTAAGACCGCAGAGCAACCCCTCCAAGAAAA	2026
1981	QY		GATCTTGGCCCTCTCTTCCCAACCGAAAGAGAGACACCCAAACTGTTTAAAACTCTCCTA	2040
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2041	QY		GGAGGCCACAGAAAAAGCAAGTCTTTGCAAGACTACTCAAATTTGAAGCGAGACGACGACT	2100
2087	DB		GGAGGCCACAGAAAAAGCAAGTCTTTGCAAGACTACTCAAATTTGAAGCGAGACGACGACT	2146
2101	QY		CAGAAGAAAGAAATTTCTGAAGGAGGAGAGAGAAAGAAATGAAGATATAACAA	2160
2147	DB		CAGAAGAAAGAAATTTCTGAAGGAGGAGAGAGAAAGAAATGAAGATATAACAA	2206
2161	QY		AAAGAAATGAAGATAAACAAAAAGAAAAATGAAGATAAGGAAAGAAAAATGAAGATAAA	2220
2207	DB		AAAGAAATGAAGATAAACAAAAAGAAAAATGAAGATAAGGAAAGAAAAATGAAGATAAA	2266
2221	QY		GATTAAGGAGAGAGCCAGAGAGAAAGCCACTGGACAGACTGAATCTGACAGCAAGTCCT	2280
2267	DB		GATTAAGGAGAGAGCCAGAGAGAAAGCCACTGGACAGACTGAATCTGACAGCAAGTCCT	2326
2281	QY		ATTGCAGTGGAGGAAGAACCCCACTCAGTTTAGAAGGACAGTTTTACCCAGAGGCACTTCT	2340
2327	DB		ATTGCAGTGGAGGAAGAACCCCACTCAGTTTAGAAGGACAGTTTTACCCAGAGGCACTTCT	2386
2341	QY		CGTCAATCACTCATTATCAGCATGGCTCTTCTGCTGAGGCGGAGAGAGGTTCTTTACT	2400
2387	DB		CGTCAATCACTCATTATCAGCATGGCTCTTCTGCTGAGGCGGAGAGAGGTTCTTTACT	2446
2401	QY		ATTGAAGTCAAGAAAAAGGCTTAAGCAATAA	2430
2447	DB		ATTGAAGTCAAGAAAAAGGCTTAAGCAATAA	2476

RESULT 2	AF228520	2135 bp	linear	PRI 30-JUN-2000
LOCUS	AF228520			
DEFINITION	Homo sapiens cone photoreceptor cGMP-gated cation channel beta-subunit (CNGB3) mRNA, complete cds.			
ACCESSION	AF228520			
VERSION	AF228520.1			
				GI:8843947

KEYWORDS	SOURCE	ORGANISM
		Homo sapiens (human)
		Homo sapiens
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE		1 (bases 1 to 2135)
AUTHORS		Sundin,O.H., Yang,J.M., Li,Y., Zhu,D., Hurd,J.N., Mitchell,T.N., Silva,E.D. and Maumenee,I.H.
TITLE		Genetic basis of total colourblindness among the Pingelapese islanders
JOURNAL		Nat. Genet. 25 (3), 289-293 (2000)

PUBMED
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 2 (bases 1 to 2135)
 SUNDIN, O.H., YANG, J.-M., LI, Y., ZHU, D., SILVA, E.D. and
 MAUMENE, I.H.
 Direct Submission
 Submitted (25-JAN-2000) Ophthalmology, Johns Hopkins School of
 Medicine, 600 North Wolfe Street, Baltimore, MD 21287, USA
 Location/Qualifiers
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ORIGIN

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QY	460	GATCTCTCTCCAGCGAGCCGACAAACTGCTCAAGGCCACGGCTGTACCAACCACTA	519	
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QY	580	AAGATGCTCTTAAACAGAGTACTTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATAC	639	
Db	241	AAGATGCTCTTAAACAGAGTACTTAAAGCGAATTAAACTTCCAAACAGCATAGATTCATAC	300	
QY	640	ACAGATCGACTCTATCTCTGTGCTCTTGTGCTCTTGTGCTATAACTTGGAACTGC	699	
Db	301	ACAGATCGACTCTATCTCTGTGCTCTTGTGCTCTTGTGCTATAACTTGGAACTGC	360	
QY	700	TGGTTTATACACCTGCGGCTCGTCTCCCATATCAACCGCAGACACATACACTACTG	759	
Db	361	TGGTTTATACACCTGCGGCTCGTCTCCCATATCAACCGCAGACACATACACTACTG	420	
QY	760	CTTATTTGGGACATCATATGTGATATCATCTACCTTTTATGCTATTTTATCCAGGCC	819	
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QY	820	AGACTCCAGTTTGTAAAGAGGAGGACATAATAGTGGATTCAAAATAGCTAAGGAAACAC	879	
Db	481	AGACTCCAGTTTGTAAAGAGGAGGACATAATAGTGGATTCAAAATAGCTAAGGAAACAC	540	
QY	880	TACAGGACTTCTACAAAATTTTCAGTTGGATGCGCATCAATAATACCATTTTGATATTTC	939	
Db	541	TACAGGACTTCTACAAAATTTTCAGTTGGATGCGCATCAATAATACCATTTTGATATTTC	600	
QY	940	TACCTCTCTTTGGGTTTAAATCCCAATGTTTAGAGCAAAATAGGATGCTTAAAGTACACTTCA	999	
Db	601	TACCTCTCTTTGGGTTTAAATCCCAATGTTTAGAGCAAAATAGGATGCTTAAAGTACACTTCA	660	
QY	1000	TTTTTTGAATTTAATCATCAGCTCTAATATGGCAAGGACATATATCTACAGAGTT	1051	

[illegible]

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Db	1786	AAAGAAAAATGAAGATAAAACAAAAAGAAAAATGAAGATAAAACAAAAAGAAAAATGAAGATAAA	1845		
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Qy	2380	GGCGGAGAGAGAGTCTTACTATTGAAGTCAAAAGAAAAAGGCTTAAGCAATAA	2430		
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RESULT 3	AF490511	2826 bp	mRNA	linear	MAM 31-JUL-2002
LOCUS	Canis familiaris cyclic nucleotide gated channel beta subunit				
DEFINITION	(CNGB3) mRNA, complete cds.				
ACCESSION	AF490511				
VERSION	AF490511.1 GI:22023792				
KEYWORDS					
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Bukaryoza; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.				
AUTHORS	1 (bases 1 to 2826) Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M., Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.				
TITLE	Canine CNGB3 mutations establish cone degeneration as orthologous to the human achromatopsia locus ACHM3				
JOURNAL	Hum. Mol. Genet. 11 (16), 1823-1833 (2002)				
PUBMED	12140185				
REFERENCE	2 (bases 1 to 2826) Sidjanin,D.J., Lowe,J.K., McElwee,J.L., Milne,B.S., Phippen,T.M., Sargan,D.R., Aguirre,G.D., Acland,G.M. and Ostrander,E.A.				
AUTHORS	Direct Submission				
TITLE	Submitted (05-MAR-2002) Baker Institute, Cornell University, Hungerford Hill Rd., Ithaca, NY 14853, USA				
JOURNAL	Location/Qualifiers				
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ORIGIN

Query Match	69.2%	Score 1682.2	DB 4	Length 2826	
Best Local Similarity	83.6%	Pred. No. 2.4e-286			
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Qy	138	CAAAAGGTGAAGAGAAATCTCT	CAAAACCAAGTCAACTCCAGT	CAAGTCTGAAGAGCCACA	197
Db	144	CAAAAGTGAAATTAATCTCT	CCTCCAAACCAAGATGACT	CCAGTCCAGTCTGAAGAATCACA	203
Qy	198	CACCAACATACAGACAAATCTCT	CCAGNAAAATTCCTCTGGAGAT	CTGACCCACAAACCC	257
Db	204	TGCCAAAATGCAAGATAAAATCT	CCGAGAAAAATTCATCTAGAGAC	CTTGACGACAAATATCC	263
Qy	258	TGACCCCTCAAAATGCGACAGAA	CAAACTGGAAACAGTCCAGAGCAG	AGAGAAATGGAACCC	317
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Qy	318	CGGAAAGAAAGGTCCAAACAG	CCCAAAACAAACCGCGCTGCAG	CTCTGTATTAATATGA	377
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Qy	378	GTATGCCGATGCCAGCTACCA	CAACCTGGTGAAGAAGATGGT	CANAGNACAGCCCTCTA	437
Db	384	GTATGCTGATGCTCAGCTAC	CAACACCTGGTGAAGAAGATGGT	CANAGAAATGCTCTA	443
Qy	438	CAAGAAAAGTTGGTAGAGGAG	ATCTCTCTCAACCCGAGAGC	CAAGCCCAAACTGCAAA	497
Db	444	TAGAAAAGTTGGCAGAGAG	ATATCTCCTCAGCTAGCC	CCCAAACTGCAAA	503
Qy	498	GCCACAGGCTGTACCAACAG	TAAAGAAAGCGATGATAAG	CCAA---CAGAACATTA	554
Db	504	GCCACAGCCGTACCATAAC	ACAGAGCAAGCAATGCTAAG	CTAATAAAGAGAACATTA	563
Qy	555	CAGGCTGTGTGGTTCAAG	GTCAAAAGATGCTTTAACAG	AGTACTTTAAAGCGAATTA	614
Db	564	TCACATATGTGTTTTAAAT	TCCAGAGATGCTCTGACAG	ATACCTTAAACGATTTAG	623
Qy	615	ACTTCCAAACAGCAGATTA	TCATACACAGATCGACTCT	ATCTCTCTGTGGCTCTTG	674
Db	624	ACTTCCAGGAGCAGATTA	TCATACACAGATCGACTCT	ATCTCTGTGGCTCTTG	683
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Db	684	CACCAATTGCTATAACTG	GAACCTGCTGCTTATACCA	CTGACCTGCTCTTCTCCATATCA	743
Qy	735	AACCGCAGACACATACACT	ACTGCTTTATTGCGACATCAT	ATCTGATATCATCTACT	794
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Qy	795	TTATGATATGCTATTAT	TCCAGCCAGACTCCAGTTT	GTGAAGAGGAGAGACATATAGT	854
Db	804	TTGTGATATGCTATTAT	TCCAGCCAGACTCCAGTTT	TATAAAGGAGGAGACATATAGT	863
Qy	855	GGATTCAAATGAGCTAAG	GAACACATACAGGACTCT	ACAAAATTTTCAGTTGGATGTCG	914
Db	864	GGATTCAAATGAGTTAA	AGAGACATACAGGAGCTCT	ACAAAATTTTCAGTTGGATGTTGC	923
Qy	915	ATCAATATATACCAAT	TGATATTGCTTACCTCT	CTTTTGGGTTTAATCCAATGTTTAGAGC	974
Db	924	GTACGATATGCCAAT	TGATGTTTTTACCTCT	CTTTTGGGTTTAATCCAATGTTTAGGAT	983
Qy	975	AAATAGGATGTTAAAG	TACACTTCATTTTTTTCGAA	TTTTTAATCATCACTAGAGTCTATAAT	103
Db	984	GAATAGGATGTTAAAG	TACACTTCATTTTTTTCGAA	TTTTTAATCATCACTAGAGTCTATAAT	104

Qy	1035	GGCAAAAGCATATATCTACAGAGTTATTTCGAAACAACCTGGATACTTCTGCTGTTTATCTCTGCA	1099
Db	1044	GGCAAAAGGCATATATCTACAGAGTCAATTCGAAACAACCTGGATACTTCTGCTATATACTCTGCA	1103
Qy	1095	CATTAAATGCTGTGTTTATTACTTGGGCTTCAAACATATGAAGAAATTTGGCACTACTAGATG	1154
Db	1104	CATTAAATGCTGTATTTATTCTGGCTTCTGACTATGAAGAAATTTGGAAGTACTAAATG	1163
Qy	1155	GGTGATATGATGGGGAAAGGAAACGAGTATCTGAGATGTTTATTATTGGGCAAGTTTCGAACCTTT	1214
Db	1164	GGTGATATAACCGTGAAGGAAACAAGTATCTAAGATGTTTATTATTGGGCTGTTCGAACCTTT	1223
Qy	1215	AAATTACCATTTGGTGGCTTCCAGAACCAAACTTATTTTGAATTTGTTTTTCAACCTTT	1274
Db	1224	AAATTACCATTTGGGGGCTTCCAGAACCAAAACATCATTTTGAATTTGTTTTTCAACCTGTT	1283
Qy	1275	GAATTTTTTTCTCGAGTTTTTTGTGTGTTCTCCAGTTTAAATTTGGTCAGATGAGAGATGTGAT	1334
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Qy	1335	TGGAGCAGCTACAGCCAAATCAGAACTACTTCCGCGCTCGATGGATGAGACCAATTCGCCTA	1394
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Qy	1395	CATGAACAATTACTCATTCTCTAAACTTGTGCAAAAGCGAGTTTCGACATCTGGTATCAATA	1454
Db	1404	CATGAACACTTATTCCATTCTAAGAAATGTGCAGAAATTCGGGTTTCGACATCTGGTATCAATA	1463
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Db	1944	TCTTAAAGAAAGGCTCCGGCCACAGAGACAAACCCCTTCCAAAGAAAGGACTTTGCCCTTTCT	2003
Qy	1995	CTTCCGACCGAAGAGAGACACCCAACTGTTTAAAACCTCTCTAGGAGGCAACAGGAAA	2054
Db	2004	CTTCCGACCGAAGAGAGACACCCAAATTTTAAAAGCTCTCTCTGGAGGTCACAGGAAA	2063
Qy	2055	AGCAAGTCTTTCAGAGCTACTCTAAATTTGAAGCGAGACCAAGCTCTCAGAAAGAAA	2111
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Db 1874 AGCTGATGTTGGTGGCCCAAGGTTTGGCAATCTTTTAACTCTGACAAAAGACTTCCA 1933
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RESULT 5

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LOCUS Q0716885 1350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 2819 from Patent WO02068579.
ACCESSION Q0716885
VERSION Q0716885.1 GI:42277742
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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REFERENCE 1

Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof

JOURNAL

Patent: WO 02068579-A 2819 06-SEP-2002;

PE Corporation (NY) (US)

FEATURES

source

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ORIGIN

Query Match 35.1%; Score 853.4; DB 6; Length 1350;
Best Local Similarity 99.9%; Pred. No. 2.6e-140;
Matches 854; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTTTAAATCGCTGACAAAGTCAACAAGTCAAGGCTATAGGAGAGAAACAATGAGAAT 60

Db 1 ATGTTTAAATCGCTGACAAAGTCAACAAGTCAAGGCTATAGGAGAGAAACAATGAGAAT 60

Qy 61 GAACAAAGTTCTCGTCCGAAATGAAGAGGCTCTCACCCCAAGTAATCATGTCAGCAAAACC 120

Db 61 GAACAAAGTTCTCGTCCGAAATGAAGAGGCTCTCACCCCAAGTAATCATGTCAGCAAAACC 120

QY	121	ACAGCACAGAGAGAAACAAAGGTGAAGAGAAATCTCTCAAAACCAAGTCAACTCCAGTC	180
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Db	181		
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Db	241		
QY	301	CAGAGGAAATGAGCCCCGGGAAAGGTGCMAACAGCCCAAAACCAAAACCCCTGCA	360
Db	301		
QY	361	GCTCTCTGTTATAATGAGTATGCCGATGCCAGCTACACAACTGGTGAAGAGTACGCT	420
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QY	421	CAAGAACAGCCCTCTACAAAGAAAAGTTGGTAGAGGAGATCTCTCTCACCCGAAAGCC	480
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QY	481	AGCCCAAACTGCAAGCCAGCGCTGTACACACAGTAAAGAAAGCGATGATAGCCA	540
Db	481		
QY	541	ACAGAACATTACTACAGGCTGTGTGGTTCAAGTCAAAAGATGCTTTACACAGATAC	600
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QY	601	TTAAAGCGAATTAACCTTCAAAACAGCAGATAGATTATACACAGATCGACTCTATCTCTG	660
Db	601		
QY	661	TGGCTCTGCTGTGCTCTGCTTAACTGGAATCTGGAATCTGCTGTTTATACACTGGCCCTC	720
Db	661		
QY	721	GTCCTTCCCATATCAAAACCGCAGACATACACTACTGCTTATTCGGACATCATATGT	780
Db	721		
QY	781	GATATCATCTACCTTTATGATATGCTATTATCCAGCCAGACTCCAGTTTGTGAAGAGA	840
Db	781		
QY	841	GGAGACATAATAGTG	855
Db	841		

RESULT 6
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LOCUS Homo sapiens clone hRNC2a retinal rod cyclic nucleotide-gated cation channel gene, complete cds.
DEFINITION L15297
ACCESSION L15297.1 GI:291914
VERSION cyclic nucleotide-gated cation channel; retinal protein.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3025)
AUTHORS Chen,T.Y., Peng,Y.W., Dhallan,R.S., Ahamed,B., Reed,R.R. and Yau,K.W.
TITLE A new subunit of the cyclic nucleotide-gated cation channel in retinal rods
JOURNAL Nature 362 (6422), 764-767 (1993)
PUBMED 7682292

REFERENCE	2 (bases 1 to 3025)
AUTHORS	Ahamed,B.
TITLE	Direct Submission
JOURNAL	Submitted (17-MAY-1993) Baheer Ahamed, Biomedical Engineering, Johns Hopkins School of Medicine, Baltimore, MD 21205, USA
COMMENT	Original source text: Homo sapiens DNA.
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ORIGIN

Query Match	23.8%;	Score	577.4;	DB	8;	Length	3025;
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Gaps	0;						
QY	617	TTCCAAACAGCATAGATTCATACAGATCGACTCTATCTCTCTGTGGCTCTTGGCTGTCA	676				
Db	635						
QY	677	CTCTTGGCTTATAACTGGAACTGCTGGTTTATACCACTCGCCTCGTCTTCCCATATCAA	736				
Db	695						
QY	737	CCGCAGACAACATACACTCTGGCTTATTGGCGACATCATATGTATCATCTACCTTT	796				
Db	755						
QY	797	ATGATATGCTTTATTCAGCCAGACTCCAGTTTGTGAAGAGGAGAGACATAATAGTGG	856				
Db	815						
QY	857	ATTCAAATGAGCTAAGGAAACACTACAGACTCTTCACAAAATTTTCAGTTGGATTTGGAT	916				
Db	875						
QY	917	CAATAATACCATTTGATATTTGCTACCTCTTCTTTGGGTTTAAATCCAAATGTTTAGAGCAA	976				
Db	935						
QY	977	ATAGGATGTTAAAGTACACTTCATTTTGTGAATTAATCATCATCCCTAGAGTCTATAATGG	1036				
Db	995						
QY	1037	ACAAAGCATATATCTACAGAGTTATTCGAACAACCTGGATACTTGTCTGTTTATTTCTGCACA	1096				
Db	1055						
QY	1097	TTAATGCCCTGTGTTTATTACTGGGCTTCAAACTATGAAGGAATTTGGCACTACTAGATGGG	1156				
Db	1115						
QY	1157	TGTATGATGGGAAGGAAACGAGTATCTGAGATGTTATTATTGGCCAGTTTCAACTTTAA	1216				
Db							

Qy	1097	TTAATGCCCTGCTGTTATTAATCTGGCTTCAAACTATGAAGAAATTTGCACTACTAGATGGG	1156
Db	1489	TGAATTCCTGCTCTTATTAATCTGGCATCGCCTATCAGGCGCTCGGCTCCACTCACTGGG	1548
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Qy	1337	GAGCAGCTACACCAATCAGAACTACTTCCGGCGCTGCATGATGACACCATGCTCTACA	1396
Db	1729	GGGCGCCACCGGAGACAGACTACTACCGCAGCTGCATGACACCGGTGAAGTACA	1788
Qy	1397	TGAACAAATTAATCTCCATTTCTAAACTTGTGCAAAAGCGAGTTCGGACTTGGTATGAATATA	1456
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Qy	1577	AGGGTTGTGATACACAGATGATTTATGACATGTTGCTAAGATTGAAATCCGTTCTCTATT	1636
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Db	2149	CTGGATCTGTGTTGGAGAAATAAGCTTGCTGCTGTTGGGGCGGGAACCGGCGCACGG	2208
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Db	2329	TGAGAAGCACAAATAAGCCCAAGGAGG	2355
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LOCUS			
DEFINITION			
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cd8.			
ACCESSION			
U58837			
VERSION			
U58837.1			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
Homo sapiens			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;	
Hominidae; Homo.	
REFERENCE	1 (bases 1 to 930)
AUTHORS	Ardell,M.D., Makhija,A.K., Oliveira,L., Miniou,P., Viegas-Pequignot,E. and Pittler,S.J.
TITLE	cdNA, gene structure, and chromosomal localization of human GARI (CNCG3), a homolog of the third subunit of bovine photoreceptor cGMP-gated channel
JOURNAL	Genomics 28 (1), 32-38 (1995)
PUBMED	7590744
REFERENCE	2 (bases 1 to 4033)
AUTHORS	Ardell,M.D., Aregon,I., Oliveira,L., Porche,G.E., Burke,E. and Pittler,S.J.
TITLE	The beta subunit of human rod photoreceptor cGMP-gated cation channel is generated from a complex transcription unit
JOURNAL	FEBS Lett. 389 (2), 213-218 (1996)
PUBMED	8766832
REFERENCE	3 (bases 1 to 4033)
AUTHORS	Pittler,S.J.
TITLE	Direct Submission
JOURNAL	Submitted (20-MAY-1996) Pittler S. J., Department of Biochemistry and Molecular Biology, University of South Alabama College of Medicine, 307 University Blvd, Mobile, AL 36688-0002,USA
FEATURES	Location/Qualifiers
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ACCESSION			
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VERSION			
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Hominidae; Homo.			
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AUTHORS			
TITLE			
1 (bases 1 to 4382)			
Identification of a domain on the beta subunit of the rod			
cGMP-gated cation channel that mediates inhibition by			
calcium-calmodulin			
J. Biol. Chem. (1998) In press			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
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Direct Submission			
Submitted (12-JAN-1998) Neuroscience, Johns Hopkins University			
School of Medicine, 725 N. Wolfe St., Baltimore, MD 21205, USA			
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VERSION CQ715550.1 GI:42276407	
KEYWORDS Homo sapiens (human)	
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REFERENCE 1	
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.	
TITLE Kits, such as nucleic acid arrays, comprising a majority of human exons or transcripts, for detecting expression and other uses thereof	
JOURNAL Patent: WO 02068579-A 1484 06-SEP-2002; PE Corporation (NY) (US)	
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1928	TTCCCCAGAGCATGACCGCTGACCAACCTGATGATGCTTATGCTATGGCTGTCTTCGTGG	1987	
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1 (bases 1 to 4763)			
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide P.,			
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Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J.,			
McKernan K.J., Malek J.A., Gunaratne P.H., Richards S.,			
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Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
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Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y.,			
Bouffard G.C., Blakesley R.W., Touchman J.W., Green E.D.,			
Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
Butterfield Y.S., Krzywinski M.I., Skalski U., Smallos D.E.,			
Schnerch A., Schein J.E., Jones S.J. and Marra M.A.			
Generation and initial analysis of more than 15,000 full-length			
human and mouse cDNA sequences			
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
12477932			
2 (bases 1 to 4763)			
Director MGC Project.			
Direct Submission			
Submitted (27-JAN-2003) National Institutes of Health, Mammalian			
Gene Collection (MGC), Cancer Genomics Office, National Cancer			
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
USA			
NTH-MGC Project URL: http://mgc.nci.nih.gov			
Contact: MGC help desk			
TITLE			
JOURNAL			
PUBMED			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REMARK			
COMMENT			

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AF074013
LOCUS
DEFINITION
Bos taurus cyclic nucleotide-gated channel beta subunit cd. 3090 bp mRNA linear MAM 10-OCT-2001
(CNCbeta) mRNA, complete cds.
ACCESSION
AF074013
VERSION
AF074013.1 GI:3309623
KEYWORDS
Bos taurus (cow)
ORGANISM
Bos taurus
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 3090)
Wienner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
Weyand, I.
Cyclic nucleotide-gated channels on the flagellum control Ca²⁺
entry into sperm
J. Cell Biol. 142 (2), 473-484 (1998)
9679145
REFERENCE
2 (bases 1 to 3090)
Wienner, B., Weiner, J., Middendorff, R., Hagen, V., Kaupp, U.B. and
Weyand, I.
TITLE
Direct Submission
Submitted (24-JUN-1998) IBI, FZ-Juelich, Leo-Brandt-Strasse,
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Juelich, Location/Qualifiers
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ORIGIN

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LOCUS               B.taurus mRNA for CNG4c protein.
DEFINITION          X94707
ACCESSION            X94707.1  GI:1154636
VERSION              CNG4c gene; CNG4c protein; cyclic nucleotide-gated cation channel;
KEYWORDS             modulatory subunit.
SOURCE               Bos taurus (cow)
ORGANISM             Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 Biel, M., Zong, X., Ludwig, A., Sautter, A. and Hofmann, F.
Molecular cloning and expression of the Modulatory subunit of the
cyclic nucleotide-gated cation channel
J. Biol. Chem. 271 (11), 6349-6355 (1996)
8626431
2 (bases 1 to 3253)
Biel, M.
Direct Submision
Submitted (08-JAN-1996) M. Biel, Inst. f. Pharmakologie und
Toxikologie, Technische Universitaet Muenchen, 80802 Muenchen,
Biedersteiner Strasse 29, FRG
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DEFINITION			
Bos taurus cyclic nucleotide-gated channel beta subunit 1e			
Bos taurus (CNCbeta) mRNA, complete cds.			
ACCESSION			
AF074014			
VERSION			
AF074014.1 GI:3309625			
KEYWORDS			
Bos taurus (cow)			
SOURCE			
Bos taurus			
ORGANISM			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
Pecora; Bovidae; Bovinae; Bos.			
REFERENCE			
1 (bases 1 to 3290)			
Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and			
Weyand,I.			
TITLE			
Cyclic nucleotide-gated channels on the flagellum control Caz+			

JOURNAL	entry into sperm
PUBMED	J. Cell Biol. 142 (2), 473-484 (1998)
REFERENCE	9679145
AUTHORS	2 (bases 1 to 3290)
	Wiesner,B., Weiner,J., Middendorff,R., Hagen,V., Kaupp,U.B. and
	Weyand,I.
TITLE	Direct Submission
JOURNAL	Submitted (24-JUN-1998) IBI, Fz-Juelich, Leo-Brandt-Strasse,
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